

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 15, 2004, 16:27:41 ; Search time 96.6571 Seconds
(without alignments)
33.333 Million cell updates/sec

Title: US-09-868-605-14_COPY_113_121
Sequence: 1 GLVPIHQMS 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

- 1: geneseqp1808:*
- 2: geneseqp1908:*
- 3: geneseqp20008:*
- 4: geneseqp20018:*
- 5: geneseqp20028:*
- 6: geneseqp20038:*
- 7: geneseqp20048:*
- 8: geneseqp20058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	26	3	AAV95328
2	47	100.0	30	3	AAV95327
3	47	100.0	250	2	AAW14944
4	47	100.0	325	3	AAV55321
5	47	100.0	325	3	AAV55324
6	44	93.6	329	3	AAV32278
7	44	93.6	329	3	AAV32285
8	44	93.6	329	5	AAO17734
9	44	93.6	329	5	AAU78121
10	44	93.6	332	2	AAV41078
11	41	87.2	280	2	AAV41078
12	41	87.2	329	2	AAV41076
13	38	80.9	303	4	AAU40963
14	38	80.9	303	6	ABM37482
15	37	78.7	103	7	ABO79571
16	36	76.6	261	5	ABR48788
17	36	76.6	261	5	ABU33032
18	35	74.5	252	2	AAV53916
19	34	72.3	38	4	ABW41828
20	34	72.3	38	4	ABW41828
21	34	72.3	38	4	AAW38152
22	34	72.3	38	4	ABW27077
23	34	72.3	38	4	AAW79933
24	34	72.3	38	4	AAW65230
25	34	72.3	38	4	ABG59572

26	34	72.3	38	5	ABG46955
27	34	72.3	141	4	AAW38884
28	34	72.3	238	5	ABW09140
29	34	72.3	238	5	ABW97746
30	34	72.3	254	6	ABU23605
31	34	72.3	947	5	ABW28863
32	34	72.3	975	4	AAW94369
33	34	72.3	1305	2	AAW88525
34	34	72.3	1353	2	AAW92551
35	34	72.3	1527	4	AAW39521
36	34	72.3	1554	4	AAW41307
37	34	72.3	1855	7	ADK40914
38	34	72.3	1871	6	ABW58345
39	34	72.3	1884	4	AAW63241
40	34	72.3	1884	7	ADJ68477
41	34	72.3	1884	8	ADJ66594
42	34	72.3	1885	4	AAW78839
43	34	72.3	1886	4	AAW79823
44	34	72.3	1906	6	ABW58321
45	34	72.3	3095	7	ADD18610

ALIGNMENTS

RESULT 1
AAV95328
ID AAV95328 standard; peptide; 26 AA.
AC AAV95328;
XX
XX
DT 12-SEP-2003 (revised)
DT 23-SEP-2000 (first entry)
XX
XX
DE OVA323-339-pig costimulatory molecule B7-2 epitope hybrid peptide 4.
XX
XX Co-stimulatory molecule; CD86; B7-2; pig; immunosuppressive;
XX xerotransplantation; organ transplant; vaccine; B-cell epitope;
XX T-cell epitope; ovalbumin; chicken.
XX
XX
XX Gallus sp.
XX Sus scrofa.
XX Chimeric.
FH Key location/Qualifiers
FT Peptide 1..17
FT Peptide /note="OVA323-339"
FT Peptide 18..26
/note="B7-2 amino acids 113-121"
XX
XX MO200037102-A2.
XX
XX 29-JUN-2000.
XX
XX 17-DEC-1999; 99WO-GB004200.
XX
XX 19-DEC-1998; 98GB-00027921.
XX 23-OCT-1999; 99GB-00025015.
XX
XX (MMLU-) ML LAB PLC.
XX
XX Lechler RI, Rogers NJ, Dorling A;
XX WPI; 2000-442537/38.
XX
XX Novel methods for improving tolerance to a xenograft comprising
XX immunizing a mammal with a T-cell epitope and a B-cell epitope.
XX
XX Disclosure; Page 23; slipp; English.
XX
XX The present sequence is that of chimeric peptide 4 comprising T-cell
XX epitope OVA323-339 from chicken egg albumin (ovalbumin) and a B-cell
XX epitope comprising amino acids 113-121 of pig co-stimulatory molecule
XX CC.

CC CD86 (B7-2) (see AAY95321). The invention relates to a novel strategy for
 CC inhibiting costimulation by porcine cells of human T cells, with
 CC particular importance in the context of xenotransplantation of porcine
 CC organs. Recipients are immunised with hybrid synthetic peptides, such as
 CC the present peptide, comprising a T cell epitope conjugated to sequences
 CC of the porcine costimulatory molecules CD80, CD86 or CD40. Peptides that
 CC induce antibodies specific for regions of costimulatory molecules
 CC involved in binding to their counter-receptors on human cells are capable
 CC of blocking the delivery of costimulation. Once the antibody response has
 CC been induced, the transplanted organ will recall this response due to the
 CC expression of the costimulatory molecules, thereby sustaining the
 CC response, and providing an endogenous mechanism of costimulatory
 CC blockade. The method is useful for improving the tolerance of a host to
 CC xenografts, particularly porcine pancreatic islet cells. (Updated on 12-
 CC SEP-2003 to standardise OS field)

Sequence 26 AA:
 Query Match 100.0%; Score 47; DB 3; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.012;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 GLVPIHOMS 9
 18 GLVPIHOMS 26

RESULT 2
 AAY95327
 ID AAY95327 standard; peptide; 30 AA.

AC AAY95327;
 DT 12-SEP-2003 (revised)
 DT 25-SEP-2000 (first entry)
 XX
 XX OVA323-339-pig costimulatory molecule B7-2 epitope hybrid peptide 3.
 DB
 XX
 XX Co-stimulatory molecule; CD86; B7-2; pig; immunosuppressive;
 KM xenotransplantation; organ transplant; vaccine; B-cell epitope;
 KW T-cell epitope; ovalbumin; chicken.
 XX
 XX
 OS Gallus sp.
 OS Sus scrofa.
 OS Chimeric.

Key Location/Qualifiers
 FT Peptide 1..17
 FT /note= "OVA323-339"
 FT 18..30
 FT /note= "B7-2 amino acids 109-121"

MO200037102-A2.
 29-JUN-2000.
 XX
 XX
 XX 17-DEC-1999; 99WO-GB004200.
 PF
 XX 19-DEC-1998; 98GB-00027921.
 PR
 XX 23-OCT-1999; 99GB-00025015.
 PR
 XX (MML-) ML LAB PLC.
 PA
 XX
 XX Lechler RI, Rogers NJ, Dorling A;
 PI
 XX
 XX WPI, 2000-442537/38.
 DR
 XX
 XX Novel methods for improving tolerance to a xenograft comprising
 PT immunising a mammal with a T-cell epitope and a B-cell epitope.
 XX
 XX Disclosure: Page 23; 81pp; English.
 PS
 XX
 CC The present sequence is that of chimeric peptide 3 comprising T-cell

CC epitope OVA323-339 from chicken egg albumin (ovalbumin) and a B-cell
 CC epitope comprising amino acids 109-121 of pig co-stimulatory molecule
 CC CD86 (B7-2) (see AAY95321). The invention relates to a novel strategy for
 CC inhibiting costimulation by porcine cells of human T cells, with
 CC particular importance in the context of xenotransplantation of porcine
 CC organs. Recipients are immunised with hybrid synthetic peptides, such as
 CC the present peptide, comprising a T cell epitope conjugated to sequences
 CC of the porcine costimulatory molecules CD80, CD86 or CD40. Peptides that
 CC induce antibodies specific for regions of costimulatory molecules
 CC involved in binding to their counter-receptors on human cells are capable
 CC of blocking the delivery of costimulation. Once the antibody response has
 CC been induced, the transplanted organ will recall this response due to the
 CC expression of the costimulatory molecules, thereby sustaining the
 CC response, and providing an endogenous mechanism of costimulatory
 CC blockade. The method is useful for improving the tolerance of a host to
 CC xenografts, particularly porcine pancreatic islet cells. (Updated on 12-
 CC SEP-2003 to standardise OS field)

Sequence 30 AA:
 Query Match 100.0%; Score 47; DB 3; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.015;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 GLVPIHOMS 9
 22 GLVPIHOMS 30

RESULT 3
 AAM14944
 ID AAM14944 standard; protein; 250 AA.

AC AAM14944;
 DT 17-OCT-2003 (revised)
 DT 16-JUN-1997 (first entry)
 XX
 XX
 DB Chimeric human/porcine CD86.
 KM Xenotransplantation; graft rejection; cell interaction; pig; CD86;
 KW monoclonal antibody; chimeric antibody; diagnosis.
 XX
 XX Homo; sapiens.
 OS Sus scrofa.
 OS Chimeric.

Key Location/Qualifiers
 FT Peptide 1..25
 FT /label= Sig_peptide
 FT Protein 26..250
 FT /label= Mat_protein
 FT Region 246..250
 FT /label= Histidine_tag

MO9711971-A1.
 03-APR-1997.
 XX
 XX
 XX 27-SEP-1996; 96WO-US015575.
 PF
 XX 28-SEP-1995; 95US-0004489P.
 PR
 XX 26-SEP-1996; 96US-00004489.
 PR
 XX (ALEX-) ALEXION PHARM INC.
 PA
 XX
 XX Mueller JF, Evans MU, Mueller EE, Rollins S, Rother RP, Mattis LA;
 PI
 XX
 XX WPI, 1997-212855/19.
 DR
 XX N-PSDB, AAT62939.
 XX
 XX Antibodies binding to porcine but not human cell interaction proteins -
 PT useful to treat and assay for rejection of xenografted porcine organs,

Query Match	100.0%	Score 47	DB 2	Length 250
Best Local Similarity	100.0%	Pred. No. 0.17		
Matches	9	Conservative	0	Mismatches 0; Indels 0; Gaps 0
QY	1	GLVPIRHMS 9		
DB	119	GLVPIRHMS 127		
RESULT 4				
ID	AAV95321	standard; protein; 325 AA.		
AC	AAV95321;			
DT	25-SEP-2000	(first entry)		
DE	Pig costimulatory molecule CD86 (B7-2).			
OS	Co-stimulatory molecule; CD86; B7-2; pig; immunosuppressive; xerotransplantation; organ transplant; vaccine; epitope.			
XX	Sus scrofa.			
XX	Key	Location/Qualifiers		
FT	Peptide	17..29 "peptide 9"		
FT	Peptide	21..32 "peptide 8"		
FT	Peptide	32..40 "peptide 2"		
FT	Peptide	76..88 "peptide 10"		
FT	Peptide	81..90 "peptide 1"		
FT	Peptide	94..104 "peptide 5"		
FT	Peptide	109..121 "peptide 3"		
FT	Peptide	113..121 "peptide 4"		
FT	Peptide	151..162 "peptide 6"		
XX	MO300037102-A2.			
XX	29-JUN-2000.			
XX	17-DEC-1999;	99MO-GB004200.		
XX	19-DEC-1998;	98GB-00027921.		
XX	23-OCT-1999;	99GB-00025015.		
XX	(MIML-) ML LAB PLC.			

PI	LechleerR1, Rogers NJ, Dorring A;
XX	
XX	WP1; 2000-442537/38.
DR	N-PSDB; AAA49661.
XX	
XX	Novel methods for improving tolerance to a xenograft comprising
PT	immunizing a mammal with a T-cell epitope and a B-cell epitope.
XX	
PS	Disclosure; Fig 6; 81pp; English.
XX	
CC	The present sequence is that of pig co-stimulatory molecule CD86 (B7-2),
CC	as deduced from an isolated cDNA clone (see AAA49661). CD86 plays a key
CC	role in T cell costimulation. The invention relates to a novel strategy
CC	for inhibiting costimulation by porcine cells of human T cells, with
CC	particular importance in the context of xerotransplantation of porcine
CC	organs. Recipients are immunized with hybrid synthetic peptides
CC	comprising a T cell epitope conjugated to sequences of the porcine
CC	costimulatory molecules CD80, CD86 or CD40, such as peptides 1-10 of CD86
CC	(see also AA95325-33). Peptides that induce antibodies specific for
CC	regions of costimulatory molecules involved in binding to their counter-
CC	receptors on human cells (CD28 and CD14) are capable of blocking the
CC	delivery of costimulation. Once the antibody response has been induced,
CC	the transplanted organ will recall this response due to the expression of
CC	the costimulatory molecules, thereby sustaining the response, and
CC	providing an endogenous mechanism of costimulatory blockade. The method
CC	is useful for improving the tolerance of a host to xenografts,
XX	particularly porcine pancreatic islet cells
XX	
SQ	Sequence 325 AA;
Query Match	100.0%; Score 47; DB 3; Length 325;
Best Local Similarity	100.0%; Pred. No. 0.23;
Matches 9; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1 GLVPIHOMS 9
DB	113 GLVPIHOMS 121
RESULT 5	
AA95324	
ID	AA95324 standard; protein; 325 AA.
XX	
AC	AA95324;
XX	
DT	25-SEP-2000 (first entry)
XX	
DE	Human costimulatory molecule CD86 (B7-2).
XX	
KM	Co-stimulatory molecule; CD86; B7-2; human; immunosuppressive;
KM	xerotransplantation; organ transplant; vaccine; epitope.
XX	
OS	Homo sapiens.
XX	
FT	Key
FT	Peptide
FT	Location/Qualifiers
FT	19..42
FT	/note= "epitope"
FT	Peptide
FT	53..73
FT	/note= "epitope"
FT	101..129
FT	/note= "epitope"
FT	136..165
FT	Peptide
FT	/note= "epitope"
XX	
PN	WO200037102-A2.
XX	
PD	29-JUN-2000.
XX	
PF	17-DEC-1999; 99WO-GB004200.
XX	
PR	19-DEC-1998; 98GB-00027921.
XX	
PR	23-OCT-1999; 99GB-00025015.
XX	

PA	(MLML-) ML LAB PLC.
PX	
PI	Lechler RI, Rogers NU, Dorling A;
XX	WPI; 2000-442537/38.
DR	
PX	
PT	Novel methods for improving tolerance to a xenograft comprising
XX	immunizing a mammal with a T-cell epitope and a B-cell epitope.
PS	
XX	Disclosure; Fig 26; 81pp; English.
CC	
CC	The present sequence is that of human co-stimulatory molecule CD86 (B7-
CC	2). CD86 plays a key role in T cell costimulation. The invention relates
CC	to a novel strategy for inhibiting costimulation by porcine cells of
CC	human T cells, with particular importance in the context of
CC	xenotransplantation of porcine organs. Recipients are immunised with
CC	hybrid synthetic peptides comprising a T cell epitope conjugated to
CC	sequences of the porcine costimulatory molecules CD80, CD86 or CD40 (see
CC	AAV9521-24). Peptides that induce antibodies specific for regions of
CC	costimulatory molecules involved in binding to their counter-receptors on
CC	human cells (CD28 and CD14) are capable of blocking the delivery of
CC	costimulation. Once the antibody response has been induced, the
CC	transplanted organ will recall this response due to the expression of the
CC	costimulatory molecules, thereby sustaining the response, and providing
CC	an endogenous mechanism of costimulatory blockade. The method is useful
CC	for improving the tolerance of a host to xenografts, particularly porcine
CC	pancreatic islet cells
CC	
XX	
SQ	Sequence 325 AA;
Query Match	100.0%; Score 47; DB 3; Length 325;
Best Local Similarity	100.0%; Pred. No. 0.23;
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	1 GLVPFHQMS 9
Db	113 GLVPFHQMS 121
RESULT 6	
AAY32278	
ID	AAY32278 standard; protein; 329 AA.
XX	
AC	AAY32278;
XX	
DT	12-SEP-2003 (revised)
DT	15-FEB-2000 (first entry)
XX	
DE	Cat CD86 (B7-2) ligand.
XX	
KM	CD86; B7-2; ligand; cat; vaccine; feline immunodeficiency virus; FIV;
KM	feline leukemia virus; feline infectious peritonitis virus;
KM	feline panleukopenia virus; feline calicivirus; feline reovirus-3;
KM	feline rotavirus; feline coronavirus; feline syncytial virus;
KM	feline sarcoma virus; feline herpesvirus; feline borna disease;
KM	rabies virus; chlamydia; Toxoplasmosis gondii; Dirofilaria immitis;
XX	parasite; autoimmune disease; transplant rejection; therapy.
OS	Felis catus.
XX	
PN	MO9957271-AA2.
XX	
PD	11-NOV-1999.
XX	
PF	30-APR-1999; 99WO-US009502.
XX	
PR	01-MAY-1998; 98US-00071699.
XX	
PA	(TEXA) TEXAS A & M SYSTEM.
XX	
FI	Collison EW, Hash SM, Choi I;
DR	WPI; 2000-052972/04.

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DR  N-PSDB; AA234785.
XX  Novel feline proteins used to produce feline vaccines which prevent
PT  infectious disease or to promote growth in homologous or heterologous
PT  species.
XX
XX  Example 1A; Fig 3A; 186pp; English.
XX
XX  The present sequence represents feline CD86 (B7-2) ligand, as predicted
CC  from isolated cDNA of peripheral blood mononuclear cells. The
CC  coexpression of CD86 with the costimulatory molecules CD28 (see AA932279)
CC  and a tumour antigen or an antigen from a pathogenic organism has the
CC  ability to activate or enhance activation of T-lymphocytes. Coexpression
CC  of CD86 with CTLA-4 (see AA932280) has the ability to regulate activation
CC  of T-lymphocytes. The invention provides isolated nucleic acids encoding
CC  feline CD86 ligand, feline CD80 (B7-1) ligand, feline CD28 receptor or
CC  feline CTLA-4 (CD152) receptor, as well as vectors comprising the nucleic
CC  acids, and polypeptides encoded by the nucleic acids. It also provides
CC  vaccines comprising the CD80, CD86, CD28 or CTLA-4 polypeptides and
CC  further comprising immunogens derived from pathogens, especially feline
CC  immunodeficiency virus (FIV), feline leukaemia virus, feline infectious
CC  peritonitis virus, feline panleukopenia virus, feline calicivirus,
CC  feline reovirus-3, feline rotavirus, feline coronavirus, feline syncytial
CC  virus, feline sarcoma virus, feline herpesvirus, feline borra disease
CC  virus, rabies virus, chlamydia, Toxoplasmosis gondii, Dirofilaria
CC  immitis, or a flea, bacterial pathogen, or parasite (all claimed).
CC  Vaccines capable of enhancing an immune response, and vaccines capable of
CC  suppressing an immune response (suitable for treating an autoimmune
CC  disease or tissue or organ transplant rejection) are claimed. (Updated on
CC  12-Sep-2003 to standardise OS field)
XX
XX  Sequence 329 AA;
SQ
Query Match          93.6%; Score 44; DB 3; Length 329;
Best Local Similarity 88.9%; Pred. No. 1;
Matches      8; Conservative      1; Mismatches      0; Indels      0; Gaps      0.
Cy      1  GTPVHQMS 9
Db      120  GLVPHQMS 128

RESULT 7
AA932285
ID  AA932285 standard; protein; 329 AA.
XX
XX  AA932285;
XX
XX  12-SEP-2003 (revised)
DT  28-FEB-2000 (first entry)
XX
XX  Feline CD86 (B7-2).
DE
XX
XX  CD86; B7-2; feline; cat; recombinant virus; vaccine; immunomodulator;
KW  tumour; cancer; therapy.
XX
XX  Felis catus.
OS
XX  WO9957295-A1.
XX  FN
XX  PD  11-NOV-1999.
XX
XX  30-APR-1999; 99WO-US009504.
XX
XX  01-MAY-1998; 98US-00071711.
XX
XX  (SCHE ) SCHERING-PLOUGH LTD.
PA  (SCHE ) SCHERING-PLOUGH VETERINARY CORP.
XX
XX  Winslow BJ, Cochran MD;
XX
XX  WPI; 2000-062155/05.
DR  N-PSDB; AA234838.

```


XX Novel recombinant virus useful as immunomodulators, particularly in
PT vaccines.
XX
XX Disclosure; Fig 3A; 230pp; English.
XX
CC This sequence represents feline CD86 (B7-2), as deduced from peripheral
CC blood mononuclear cell cDNA (see A234835). Manipulating the expression
CC of CD28 or CTLA-4 (and/or their co-stimulatory ligands CD80 and CD86)
CC regulates T cell proliferation and cytokine release. The invention
CC relates to a recombinant virus that contains at least one foreign nucleic
CC acid, inserted into a nonessential genomic region, that encodes feline
CC CD28, CD80, CD86 or CTLA-4 protein, or their immunogenic fragments, and
CC is expressed when the recombinant virus is introduced into a suitable
CC host. The invention also provides a recombinant virus further comprising
CC a foreign nucleic acid encoding an immunogen derived from a feline
CC pathogen; recombinant viruses capable of enhancing an immune response to
CC protect against disease; recombinant viruses expressing antisense
CC sequences, capable of suppressing an immune response in a feline, e.g.,
CC for treatment of autoimmune disease or transplant rejection; and
CC recombinant viruses expressing DNA encoding CD80 and/or CD86 used to
CC reduce or eliminate a tumour in cats. (Updated on 12-SEP-2003 to
CC standardise OS field)
CC
SQ Sequence 329 AA:

Query Match 93.6%; Score 44; DB 3; Length 329;
Best Local Similarity 88.9%; Pred. No. 1;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLVPIHOMS 9
|||:||||
120 GLVPMHOMS 128

Db

RESULT 8
AA017734
ID AA017734 standard; protein; 329 AA.
XX
AC AA017734;
XX
DT 08-AUG-2002 (first entry)
XX
DE Feline CD86.
XX
KW Cat; CD28; CD80; CTLA-4; CD86; immunogen; vaccine; viral infection;
KW feline immunodeficiency disease; feline infectious peritonitis;
KW feline leukemia virus; cancer; degenerative disease; autoimmune disease;
KW virucide; immunomodulator; cytostatic; immunodeficiency.
XX
OS Felis catus.
XX
PN US2002051792-A1.
XX
PD 02-MAY-2002.
XX
PF 30-APR-1999; 99US-00303040.
XX
PR 01-MAY-1998; 98US-0083870P.
XX
PA (WINS/) WINSLOW B J.
PA (COCH/) COCHRAN M D.
XX
PI Winslow BJ, Cochran MD;
XX
DR WPI; 2002-415200/44.
DR N-PSDB; AAL46840.
XX
PT New recombinant virus, useful for immunizing felines to prevent or treat
PT feline immunodeficiency virus, comprises foreign nucleic acid encoding
PT feline cytotoxic T lymphocyte accessory molecules CD28, CD80, CD86 or
PT CTLA-4.
XX

P5 Disclosure; Fig 3; 77pp; English.
XX
CC The present invention relates to a recombinant virus comprising at least
CC one foreign nucleic acid encoding a protein selected from feline
CC cytotoxic T lymphocyte accessory molecules CD28, CD80, CD86 or CTLA-4,
CC which is capable of expression when the virus is introduced into an
CC appropriate host. The virus can be administered to the feline in order to
CC elicit or enhance an immune response to prevent or treat feline
CC immunodeficiency disease, feline leukemia, feline infectious peritonitis,
CC cancers, degenerative and autoimmune diseases and immunodeficiency. The
CC present sequence is a cytotoxic T lymphocyte accessory molecule described
CC in the exemplification of the invention
XX
SQ Sequence 329 AA:

Query Match 93.6%; Score 44; DB 5; Length 329;
Best Local Similarity 88.9%; Pred. No. 1;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLVPIHOMS 9
|||:||||
120 GLVPMHOMS 128

Db

RESULT 9
AAU78121
ID AAU78121 standard; protein; 329 AA.
XX
AC AAU78121;
XX
DT 02-JUN-2002 (first entry)
XX
DE Feline CD86 protein.
XX
KW Cat; vaccine; feline immunodeficiency virus; FIV; immunosuppressant;
KW feline infectious peritonitis; CD80 ligand; CD86 ligand; CD28; receptor;
KW CTLA-4; vaccine; rabies; autoimmune disease; organ transplant;
KW toxoplasmosis gondii; flea; parasite; panleukopenia; feline leukemia;
KW Feline; calicivirus; rotavirus; reovirus type 3; coronavirus; herpes;
KW borna disease.
XX
OS Felis sp.
XX
PN US2002028208-A1.
XX
PD 07-MAR-2002.
XX
PF 30-APR-1999; 99US-00303510.
XX
PR 01-MAY-1998; 98US-0083869P.
XX
PA (COLL/) COLLISSON E W.
PA (HASH/) HASH S M.
PA (CHOI/) CHOI I.
XX
PI Collisson EW, Hash SM, Choi I;
XX
DR WPI; 2002-315045/35.
DR N-PSDB; ABX48230.
XX
PT Polynucleotide encoding polypeptide of CD80 ligand, CD86 ligand, CD28
PT receptor or CTLA-4 receptor as vaccine for inducing immune response in
PT feline suffering from autoimmune disease or tissue or organ transplant.
XX
PS Disclosure; Fig 3A; 73pp; English.
XX
CC This invention relates to the DNA and protein sequences encoding a
CC soluble CD80 ligand, soluble CD86 ligand, soluble and membrane-bound CD28
CC receptor and soluble or membrane bound CTLA-4 receptor. The invention
CC also relates to a vaccine comprising an effective amount of these
CC receptor proteins. A vaccine is useful for inducing immunity or enhancing
CC an immune response in a cat. The protein sequences of the invention are
CC useful for suppressing an immune response in a feline suffering from an

CC autoimmune disease or the recipient of a tissue or organ transplant. A
 CC vector containing an immune response in a feline to an immunogen such as rabies
 CC virus, chlamydia, toxoplasmosis gondii, flea, feline immunodeficiency
 CC virus, feline leukaemia virus, calicivirus, reovirus type 3, rotavirus,
 CC (FIP), panleukopenia virus, herpes virus, sarcoma virus, borna disease
 CC coronavirus, syncytial virus, measles virus, may be further utilised to
 CC virus or a parasite. The protein sequences may be further utilised to
 CC promote growth in homologous or heterologous feline species. Enhancement
 CC of immunity through the interaction of soluble CD80 or soluble CD86 with
 CC CD28 or CTLA-4 or inhibition of an immune response through the
 CC interaction of feline CD80 or CD86 with CTLA-4 takes advantage of the
 CC natural process of regulation rather than adding foreign substances that
 CC could have multiple, even detrimental effects on overall or long term
 CC health. The present sequence represents feline CD86 protein of the
 CC invention

CC SQ Sequence 329 AA;

CC Query Match 93.6%; Score 44; DB 5; Length 329;
 CC Best Local Similarity 88.9%; Pred. No. 1;
 CC Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

CC QY 1 GIVPWHQMS 9
 CC |||||:
 CC Db 120 GIVPWHQMS 128

CC RESULT 10
 CC AAY41079
 CC ID AAY41079 standard; protein; 332 AA.
 CC AC AAY41079;
 CC XX 20-DEC-1999 (first entry)
 CC DT
 CC XX
 CC DE Feline B7-2 protein.
 CC XX
 CC KM B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
 CC KM allergic reaction; infectious disease; tumor development; canine;
 CC KM graft rejection; inflammation; arthritis; atopic dermatitis; se.
 CC XX
 CC OS Felis catus.
 CC XX
 CC PN WO9947558-A2.
 CC XX
 CC PD 23-SEP-1999.
 CC XX
 CC PF 19-MAR-1999; 99WO-US006187.
 CC XX
 CC PR 19-MAR-1998; 98US-0078765P.
 CC XX
 CC PR 17-APR-1998; 98US-00062597.
 CC XX
 CC PA (HESK-) HESKA CORP.
 CC XX
 CC PI Sim G, Yang S, Sellins KS;
 CC XX
 CC DR WPI; 1999-571822/48.
 CC DR N-PSDB; AAZ27923; AAZ27931.
 CC XX
 CC PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
 CC PT treating, e.g. autoimmune and atopic diseases.
 CC XX
 CC PS Claim 4; Page 116-119; 148pp; English.
 CC XX
 CC CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)
 CC CC encoding nucleic acid molecules from dogs and cats. The proteins can be
 CC CC expressed by standard recombinant methodology. The nucleic acid molecules
 CC CC and the encoded proteins can be used for preventing or treating diseases,
 CC CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
 CC CC development, graft rejection, inflammation, arthritis and atopic diseases
 CC CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
 CC CC cats, cattle, sheep or pets. The products can also be used for detection,

CC diagnosis and drug screening

CC SQ Sequence 332 AA;

CC Query Match 93.6%; Score 44; DB 2; Length 332;
 CC Best Local Similarity 88.9%; Pred. No. 1;
 CC Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

CC QY 1 GIVPWHQMS 9
 CC |||||:
 CC Db 120 GIVPWHQMS 128

CC RESULT 11
 CC AAY41078
 CC ID AAY41078 standard; protein; 280 AA.
 CC AC AAY41078;
 CC XX 20-DEC-1999 (first entry)
 CC DT
 CC XX
 CC DE Canine B7-2S protein.
 CC XX
 CC KM B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
 CC KM allergic reaction; infectious disease; tumor development; canine;
 CC KM graft rejection; inflammation; arthritis; atopic dermatitis.
 CC XX
 CC OS Canis familiaris.
 CC XX
 CC PN WO9947558-A2.
 CC XX
 CC PD 23-SEP-1999.
 CC XX
 CC PF 19-MAR-1999; 99WO-US006187.
 CC XX
 CC PR 19-MAR-1998; 98US-0078765P.
 CC XX
 CC PR 17-APR-1998; 98US-00062597.
 CC XX
 CC PA (HESK-) HESKA CORP.
 CC XX
 CC PI Sim G, Yang S, Sellins KS;
 CC XX
 CC DR WPI; 1999-571822/48.
 CC DR N-PSDB; AAZ27921, AAZ27923.
 CC XX
 CC PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
 CC PT treating, e.g. autoimmune and atopic diseases.
 CC XX
 CC PS Claim 4; Page 109-111; 148pp; English.
 CC XX
 CC CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)
 CC CC encoding nucleic acid molecules from dogs and cats. The proteins can be
 CC CC expressed by standard recombinant methodology. The nucleic acid molecules
 CC CC and the encoded proteins can be used for preventing or treating diseases,
 CC CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
 CC CC development, graft rejection, inflammation, arthritis and atopic diseases
 CC CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
 CC CC cats, cattle, sheep or pets. The products can also be used for detection,
 CC CC diagnosis and drug screening

CC SQ Sequence 280 AA;

CC Query Match 87.2%; Score 41; DB 2; Length 280;
 CC Best Local Similarity 77.8%; Pred. No. 3.6;
 CC Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

CC QY 1 GIVPWHQMS 9
 CC |||||:
 CC Db 119 GIVPWHQMS 127

CC RESULT 12
 CC AAY41076

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ID  AA41076 standard; protein; 329 AA.
XX
XX  AA41076;
AC
XX  20-DEC-1999 (first entry)
DT
XX
XX  Canine B7-2 protein.
DE
XX
XX  B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
XX  allergic reaction; infectious disease; tumor development; canine;
XX  graft rejection; inflammation; arthritis; atopic dermatitis.
XX
XX  Canis familiaris.
OS
XX
XX  WO9947558-A2.
PN
XX
XX  23-SEP-1999.
PD
XX
XX  19-MAR-1999; 99WO-US006187.
PF
XX
XX  19-MAR-1998; 98US-0078765P.
PR
XX  17-APR-1998; 98US-00062597.
XX
XX  (HESK-) HESKA CORP.
PA
XX
XX  Sim G, Yang S, Sellins KS;
PI
XX  WPI; 1999-571822/48.
DR
XX  N-PSDB; AA227913, AA227915.
PT
XX  New isolated B7 and CTLA4 nucleic acids, used to develop products for
XX  treating, e.g. autoimmune and atopic diseases.
PS
XX  Claim 4; Page 97-99; 148pp; English.
XX
XX  The invention provides B7 and CTLA4 (T cell costimulatory proteins)
XX  encoding nucleic acid molecules from dogs and cats. The proteins can be
XX  expressed by standard recombinant methodology. The nucleic acid molecules
XX  and the encoded proteins can be used for preventing or treating diseases,
XX  e.g., autoimmune diseases, allergic reactions, infectious diseases, tumor
XX  development, graft rejection, inflammation, arthritis and atopic diseases
XX  such as atopic dermatitis. They can be used in mammals such humans, dogs,
XX  cats, cattle, sheep or pets. The products can also be used for detection,
XX  diagnosis and drug screening
XX
XX  Sequence 329 AA;
SQ

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Query Match 87.2%; Score 41; DB 2; Length 329;
 Best Local Similarity 77.8%; Pred. No. 4.3;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY  1 GLVPIHQMS 9
    |||:|:|:|
Db  119 GLVPIHQMN 127

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RESULT 13
 AAU40963
 ID AAU40963 standard; protein; 303 AA.
 XX
 XX AAU40963;
 AC
 XX
 XX 13-FEB-2002 (first entry)
 DT
 XX
 XX Propionibacterium acnes immunogenic protein #1859.
 DE
 XX
 XX SAPHO syndrome; synovitis; acne; pustulosis; hyperostosis; osteomyelitis;
 XX uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 XX inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 XX dermatological; osteopathic; neuroprotectant.
 OS
 XX Propionibacterium acnes.
 XX

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PN  WO200181581-A2.
XX
XX  01-NOV-2001.
PD
XX
XX  20-APR-2001; 2001WO-US012865.
PF
XX
XX  21-APR-2000; 2000US-0199047P.
PR
XX  02-JUN-2000; 2000US-0208841P.
XX  07-JUL-2000; 2000US-0216747P.
XX
XX  (CORI-) CORIXA CORP.
PA
XX
XX  Skeiky YW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
PI  L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX  WPI; 2001-616774/71.
DR
XX  N-PSDB; AAS59513.
PT
XX  Propionibacterium acnes polypeptides and nucleic acids useful for
XX  vaccinating against and diagnosing infections, especially useful for
XX  treating acne vulgaris.
XX
XX  Example 1; SEQ ID NO 2158; 1069pp; English.
PS
XX
XX  Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
XX  polypeptides. The proteins and their associated DNA sequences are used in
XX  the treatment, prevention and diagnosis of medical conditions caused by
XX  P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
XX  pustulosis, hyperostosis and osteomyelitis), uveitis and endophthalmitis.
XX  P. acnes is also involved in infections of bone, joints and the central
XX  nervous system, however it is particularly involved in the inflammatory
XX  lesions associated with acne vulgaris. A method for detecting the
XX  presence or absence of P. acnes in a patient comprises contacting a
XX  sample with a binding agent that binds to the proteins of the invention
XX  and determining the amount of bound protein in the sample. The
XX  polypeptides may be used as antigens in the production of antibodies
XX  specific for P. acnes proteins. These antibodies can be used to
XX  downregulate expression and activity of P. acnes polypeptides and
XX  therefore treat P. acnes infections. The antibodies may also be used as
XX  diagnostic agents for determining P. acnes presence, for example, by
XX  enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
XX  this patent did not form part of the printed specification, but was
XX  obtained in electronic format directly from WIPO at
XX  ftp.wipo.int/pub/published_pct_sequences
XX
XX  Sequence 303 AA;
SQ

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Query Match 80.9%; Score 38; DB 4; Length 303;
 Best Local Similarity 66.7%; Pred. No. 17;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY  1 GLVPIHQMS 9
    |||:|:|:|
Db  35 GLVPIHQLS 43

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RESULT 14
 ABM37482
 ID ABM37482 standard; protein; 303 AA.
 XX
 XX ABM37482;
 AC
 XX
 XX 20-OCT-2003 (first entry)
 DT
 XX
 XX Propionibacterium acnes predicted ORF-encoded polypeptide #2158.
 DE
 XX
 XX Acne vulgaris; antiseborrheic; dermatological; antibacterial;
 XX immunostimulant; immune response; vaccine.
 XX Propionibacterium acnes.
 OS
 XX WO2003033515-A1.
 XX

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OM protein - protein search, using sw model

Run on: December 15, 2004, 16:29:06 ; Search time 15.4286 Seconds

(without alignment) 38.685 Million cell updates/sec

Title: US-09-868-605-14_COPY_113_121

Perfect score: 47

Sequence: 1 GLVPIHQS 9

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
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3: /cgn2_6/prodata/1/1aa/6A-COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B-COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCITUS-COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfillset1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	325	4	US-09-651-200-20
2	44	93.6	329	4	US-09-651-200-18
3	44	93.6	329	4	US-09-303-040-6
4	41	87.2	329	4	US-09-651-200-19
5	37	78.7	103	4	US-09-252-991A-28317
6	34	72.3	1305	3	US-08-864-785-3
7	34	72.3	1353	3	US-08-894-173-2
8	34	72.3	1353	3	US-09-398-193-2
9	34	72.3	1353	3	US-09-473-717-3
10	34	72.3	1884	4	US-09-538-092-1339
11	33	70.2	249	4	US-09-270-767-4436
12	33	70.2	275	3	US-09-134-001C-3290
13	33	70.2	496	4	US-09-252-991A-31314
14	33	70.2	525	4	US-09-252-991A-28266
15	32	68.1	91	4	US-09-621-976-7293
16	32	68.1	110	3	US-08-479-744A-45
17	32	68.1	110	3	US-08-280-757B-45
18	32	68.1	110	4	US-09-425-762-45
19	32	68.1	249	4	US-10-101-664A-593
20	32	68.1	333	4	US-09-651-200-21
21	32	68.1	333	4	US-09-441-411-22
22	32	68.1	333	5	PCT-US94-09642-2
23	32	68.1	334	4	US-09-910-174B-6
24	32	68.1	334	4	US-09-620-461-6
25	32	68.1	329	2	US-08-456-104-2
26	32	68.1	329	2	US-08-101-624-2
27	32	68.1	329	3	US-08-479-744A-2

28	32	68.1	329	3	US-08-280-757B-2	Sequence 2, Appli
29	32	68.1	329	3	US-08-205-687A-23	Sequence 23, Appli
30	32	68.1	329	3	US-08-702-525-23	Sequence 23, Appli
31	32	68.1	329	3	US-08-403-253A-4	Sequence 4, Appli
32	32	68.1	329	4	US-09-667-135-32	Sequence 32, Appli
33	32	68.1	329	4	US-08-435-816A-4	Sequence 4, Appli
34	32	68.1	329	4	US-09-425-762-2	Sequence 2, Appli
35	32	68.1	329	4	US-09-837-867A-23	Sequence 23, Appli
36	32	68.1	329	4	US-09-206-132-23	Sequence 2, Appli
37	32	68.1	329	4	US-09-441-411-26	Sequence 26, Appli
38	32	68.1	329	5	PCT-US95-02576-23	Sequence 23, Appli
39	32	68.1	351	4	US-09-756-983-18	Sequence 18, Appli
40	32	68.1	392	4	US-09-710-279-1908	Sequence 1908, Ap
41	32	68.1	392	4	US-09-710-279-1908	Sequence 2758, Ap
42	32	68.1	411	3	US-09-134-001C-3121	Sequence 3121, Ap
43	32	68.1	460	4	US-09-543-681A-5773	Sequence 5773, Ap
44	32	68.1	553	4	US-09-252-991A-24465	Sequence 24465, A
45	32	68.1	872	3	US-08-337-797A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-651-200-20
; Sequence 20, Application US/09651200
; Patent No. 6429303
; GENERAL INFORMATION:
; APPLICANT: Green et al
; TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B
; TITLE OF INVENTION: Polynucleotide Activation Antigen B-7 Family and
; FILE REFERENCE: 15966-562 (CURA-62)
; CURRENT APPLICATION NUMBER: US/09/651.200
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/152383
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/172909
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 325
; TYPE: PRT
; ORGANISM: sus sp.
US-09-651-200-20
Query Match 100.0%; Score 47; DB 4; Length 325;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 113 GLVPIHQS 121
OY 1 GLVPIHQS 9
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US-09-651-200-18
; Sequence 18, Application US/09651200
; Patent No. 6429303
; GENERAL INFORMATION:
; APPLICANT: Green et al
; TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B
; TITLE OF INVENTION: Polynucleotide Activation Antigen B-7 Family and
; FILE REFERENCE: 15966-562 (CURA-62)
; CURRENT APPLICATION NUMBER: US/09/651.200
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/152383
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/172909

;; PRIOR FILING DATE: 1999-12-21
;; PRIOR APPLICATION NUMBER: 60/183578
;; PRIOR FILING DATE: 2000-02-18
;; NUMBER OF SEQ ID NOS: 25
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO: 18
;; LENGTH: 329
;; TYPE: PRT
;; ORGANISM: Felis catus
US-09-651-200-18

Query Match 93.6%; Score 44; DB 4; Length 329;
Best Local Similarity 88.9%; Pred. No. 0.22;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIVPIHOMS 9
|||:||||
DB 120 GLVPMHOMS 128

RESULT 3
US-09-303-040-6
; Sequence 6, Application US/09303040
; Patent No. 6555671
; GENERAL INFORMATION:
; APPLICANT: Winslow, Barbara J.
; APPLICANT: Cochran, Mark D.
; TITLE OF INVENTION: Recombinant Virus Expressing Foreign DNA Encoding
; TITLE OF INVENTION: Feline CD86, Feline CD86, Feline CD28, Feline CTLA-4 or
; FILE REFERENCE: 54957-B
; CURRENT APPLICATION NUMBER: US/09/303,040
; CURRENT FILING DATE: 1999-04-30
; EARLIER APPLICATION NUMBER: 60/083,870
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 6
; LENGTH: 329
; TYPE: PRT
; ORGANISM: feline CD86
US-09-303-040-6

Query Match 93.6%; Score 44; DB 4; Length 329;
Best Local Similarity 88.9%; Pred. No. 0.22;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIVPIHOMS 9
|||:||||
DB 120 GLVPMHOMS 128

RESULT 4
US-09-651-200-19
; Sequence 19, Application US/09651200
; Patent No. 6429303
; GENERAL INFORMATION:
; APPLICANT: Green et al
; TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B
; TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and
; FILE REFERENCE: 15966-562 (CURA-62)
; CURRENT APPLICATION NUMBER: US/09/651,200
; CURRENT FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/152383
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/172909
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/183578
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 19

;; LENGTH: 329
;; TYPE: PRT
;; ORGANISM: Canis familiaris
US-09-651-200-19

Query Match 87.2%; Score 41; DB 4; Length 329;
Best Local Similarity 77.8%; Pred. No. 0.97;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIVPIHOMS 9
|||:||||
DB 119 GLVPMHOMN 127

RESULT 5
US-09-252-991A-28317
; Sequence 28317, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO: 28317
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28317

Query Match 78.7%; Score 37; DB 4; Length 103;
Best Local Similarity 66.7%; Pred. No. 1.8;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIVPIHOMS 9
|||:||||
DB 61 GLTPIHQLA 69

RESULT 6
US-08-864-785-3
; Sequence 3, Application US/08864785A
; Patent No. 6329566
; GENERAL INFORMATION:
; APPLICANT: Kaplan, Joshua M.
; APPLICANT: Oppenheimer, Allison J.
; TITLE OF INVENTION: METHODS FOR THE DETECTION, TREATMENT,
; TITLE OF INVENTION: AND PREVENTION OF NEURODEGENERATION
; FILE REFERENCE: 00786/353001
; CURRENT APPLICATION NUMBER: US/08/864,785A
; CURRENT FILING DATE: 1997-05-29
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 3
; LENGTH: 1305
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-864-785-3

Query Match 72.3%; Score 34; DB 3; Length 1305;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIVPIHOMS 9
|||:||||
DB 1249 GVVPMHOLS 1257

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RESULT 7
US-08-894-173-2
; Sequence 2, Application US/08894173A
; Patent No. 6090612
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: Adenylate cyclase and uses therefor
; FILE REFERENCE: P14716C
; CURRENT APPLICATION NUMBER: US/08/894,173A
; CURRENT FILING DATE: 1997-08-13
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1353
; TYPE: PRT
; ORGANISM: Mouse
; FEATURE:
; OTHER INFORMATION: HYPOTHETICAL : NO
US-08-894-173-2

Query Match          72.3%; Score 34; DB 3; Length 1353;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLVPHQMS 9
DB 1249 GVVPHQOLS 1257

RESULT 8
US-09-398-193-2
; Sequence 2, Application US/09398193
; Patent No. 6197581
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: Adenylate cyclase and uses therefor
; FILE REFERENCE: P24360-
; CURRENT APPLICATION NUMBER: US/09/398,193
; CURRENT FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1353
; TYPE: PRT
; ORGANISM: Mouse
; FEATURE:
; OTHER INFORMATION: HYPOTHETICAL : NO
US-09-398-193-2

Query Match          72.3%; Score 34; DB 3; Length 1353;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLVPHQMS 9
DB 1249 GVVPHQOLS 1257
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; CURRENT APPLICATION NUMBER: US/09/473,717
; CURRENT FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: PCT/US98/13541
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/098,559
; PRIOR FILING DATE: 1997-07-01
; PRIOR APPLICATION NUMBER: 08/886,440
; PRIOR FILING DATE: 1997-07-01
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1353
; TYPE: PRT
; ORGANISM: murine type IX adenyl cyclase
US-09-473-717-3

Query Match          72.3%; Score 34; DB 3; Length 1353;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLVPHQMS 9
DB 1249 GVVPHQOLS 1257

RESULT 10
US-09-538-092-1329
; Sequence 1329, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Glco, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuratSeqFormatVer Version 0.9
; SEQ ID NO 1329
; LENGTH: 1884
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number Q14690
US-09-538-092-1329

Query Match          72.3%; Score 34; DB 4; Length 1884;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLVPHQMS 9
DB 580 GLVPHQELS 588

RESULT 11
US-09-270-767-44136
; Sequence 44136, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
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SEQ ID NO 44136
LENGTH: 249
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-44136

Query Match 70.2%; Score 33; DB 4; Length 249;
Best Local Similarity 75.0%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LVPIHOM 9
DB 7 MWPHTMS 14

RESULT 12
US-09-134-001C-3290
Sequence 3290, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lytta Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT FILING DATE: 1998-08-13
CURRENT APPLICATION NUMBER: US/09/134,001C
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3290
LENGTH: 275
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3290

Query Match 70.2%; Score 33; DB 3; Length 275;
Best Local Similarity 71.4%; Pred. No. 39;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 VPIHOM 9
DB 159 VPIHOM 165

RESULT 13
US-09-252-991A-31314
Sequence 31314, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUDINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT FILING DATE: 1999-02-18
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31314
LENGTH: 496
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31314

Query Match 70.2%; Score 33; DB 4; Length 496;
Best Local Similarity 55.6%; Pred. No. 78;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLVPIHOM 9

DB 250 GLVPIHOM 258

RESULT 14
US-09-252-991A-28266
Sequence 28266, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUDINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT FILING DATE: 1999-02-18
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 28266
LENGTH: 525
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28266

Query Match 70.2%; Score 33; DB 4; Length 525;
Best Local Similarity 55.6%; Pred. No. 83;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLVPIHOM 9
DB 288 GLVPIHOM 296

RESULT 15
US-09-621-976-7293
Sequence 7293, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jober, S.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT FILING DATE: 2000-07-21
CURRENT APPLICATION NUMBER: US/09/621,976
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 7293
LENGTH: 91
TYPE: PRT
ORGANISM: Homo sapiens
US-09-621-976-7293

Query Match 68.1%; Score 32; DB 4; Length 91;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LVPIHQ 7
DB 17 LVPIHQ 22

Search completed: December 15, 2004, 16:38:41
Job time: 16.4286 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 15, 2004, 16:37:44 ; Search time 87.4286 Seconds
(without alignments)
36.768 Million cell updates/sec

Title: US-09-868-605-14_COPY_113_121

Perfect score: 47
Sequence: 1 GLVPIHOMS 9

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Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	93.6	329	9 US-09-303-510-6	Sequence 6, Appli
2	44	93.6	329	9 US-09-303-040-6	Sequence 6, Appli
3	44	93.6	332	16 US-10-790-396-26	Sequence 26, Appli
4	41	87.2	280	16 US-10-790-396-17	Sequence 17, Appli
5	41	87.2	329	16 US-10-790-396-7	Sequence 7, Appli
6	37	78.7	96	17 US-10-425-115-208294	Sequence 208294,
7	37	78.7	99	15 US-10-389-647-604	Sequence 604, App
8	36	76.6	122	17 US-10-425-115-321220	Sequence 321220,
9	36	76.6	261	15 US-10-282-122A-60956	Sequence 60956, A
10	35	74.5	317	17 US-10-739-930-7964	Sequence 7964, Ap
11	34	72.3	38	9 US-09-864-761-42375	Sequence 42375, A
12	34	72.3	89	17 US-10-425-115-212035	Sequence 212035,
13	34	72.3	238	10 US-09-935-338-233	Sequence 233, App

14	34	72.3	238	15 US-10-380-430-59	Sequence 59, Appli
15	34	72.3	254	15 US-10-282-122A-51529	Sequence 51529, A
16	34	72.3	258	16 US-10-437-963-146161	Sequence 146161,
17	34	72.3	299	16 US-10-437-963-156621	Sequence 156621,
18	34	72.3	315	14 US-10-156-761-12810	Sequence 12810, A
19	34	72.3	1305	14 US-10-014-079A-3	Sequence 3, Appli
20	34	72.3	1353	9 US-09-751-100B-2	Sequence 2, Appli
21	34	72.3	1353	13 US-10-071-123-3	Sequence 3, Appli
22	34	72.3	1855	15 US-10-334-143-21	Sequence 21, Appli
23	34	72.3	1871	14 US-10-144-194A-114	Sequence 114, App
24	34	72.3	1884	16 US-10-408-765A-283	Sequence 283, App
25	34	72.3	1906	14 US-10-144-194A-88	Sequence 88, Appli
26	33	70.2	105	16 US-10-767-701-49861	Sequence 49861, A
27	33	70.2	105	17 US-10-425-115-288437	Sequence 288437,
28	33	70.2	121	16 US-10-437-963-160312	Sequence 160312,
29	33	70.2	1219	14 US-10-369-493-12135	Sequence 12135, A
30	33	70.2	228	17 US-10-425-115-344824	Sequence 344824,
31	33	70.2	268	15 US-10-282-122A-71160	Sequence 71160, A
32	33	70.2	280	15 US-10-425-114-67650	Sequence 67650, A
33	33	70.2	292	15 US-10-425-114-59810	Sequence 59810, A
34	33	70.2	407	14 US-10-369-493-16931	Sequence 16931, A
35	33	70.2	411	14 US-10-369-493-582	Sequence 582, App
36	33	70.2	429	15 US-10-282-122A-73168	Sequence 73168, A
37	33	70.2	453	15 US-10-282-122A-55853	Sequence 55853, A
38	33	70.2	453	15 US-10-282-122A-75796	Sequence 75796, A
39	33	70.2	464	15 US-10-425-114-41830	Sequence 41830, A
40	33	70.2	556	14 US-10-156-761-9809	Sequence 9809, Ap
41	33	70.2	557	15 US-10-403-571-54	Sequence 54, Appli
42	33	70.2	635	15 US-10-282-122A-53309	Sequence 53309, A
43	33	70.2	718	15 US-10-282-122A-76979	Sequence 76979, A
44	33	70.2	1181	14 US-10-199-937-139	Sequence 139, App
45	33	70.2	3583	16 US-10-437-963-125761	Sequence 125761,

ALIGNMENTS

RESULT 1
US-09-303-510-6
; Sequence 6, Application US/09303510A
; Patent No. US20020028208A1
; GENERAL INFORMATION:
; APPLICANT: Collisch, Ellen W.
; APPLICANT: Hash, Stephen M.
; APPLICANT: Choi, Insoo
; TITLE OF INVENTION: Feline CD80, Feline CD86, Feline CD28, and Feline
; TITLE OF INVENTION: CITRA-4 Nucleic Acid and Polypeptides
; FILE REFERENCE: 54954
; CURRENT APPLICATION NUMBER: US/09/303,510A
; CURRENT FILING DATE: 1999-04-30
; EARLIER APPLICATION NUMBER: 60/083,969
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Feline
US-09-303-510-6
Query Match 93.6%; Score 44; DB 9; Length 329;
Best Local Similarity 98.9%; Pred. No. 3;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 GLVPIHOMS 9
DB 120 GLVPIHOMS 128
RESULT 2
US-09-303-040-6
; Sequence 6, Application US/09303040
; Patent No. US20020051792A1

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/ GENERAL INFORMATION:
/ APPLICANT: Winslow, Barbara J.
/ APPLICANT: Cochran, Mark D.
/ TITLE OF INVENTION: Recombinant Virus Expressing Foreign DNA Encoding
/ TITLE OF INVENTION: Feline CD80, Feline CD86, Feline CD28, Feline CTLA-4 or
/ FILE REFERENCE: Feline Interferon-gamma And Uses Thereof
/ FILE REFERENCE: 54957-B
/ CURRENT APPLICATION NUMBER: US/09/303,040
/ PRIOR FILING DATE: 1999-04-30
/ EARLIER APPLICATION NUMBER: 60/083,870
/ PRIOR FILING DATE: 1998-05-01
/ NUMBER OF SEQ ID NOS: 82
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 6
/ LENGTH: 329
/ TYPE: PRT
/ ORGANISM: feline CD86
US-09-303-040-6

Query Match          93.6%; Score 44; DB 9; Length 329;
Best Local Similarity 88.9%; Pred. No. 3;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GLVPIHOMS 9
Db      120 GLVPIHOMS 128

RESULT 3
US-10-790-396-26
/ Sequence 26, Application US/10790396
/ Publication No. US20040157296A1
/ GENERAL INFORMATION:
/ APPLICANT: Sim, Gek-Kee
/ APPLICANT: Yang, Shumin
/ TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY PROTEINS, NUCLEIC
/ FILE REFERENCE: IM-1-CI-PCT
/ CURRENT APPLICATION NUMBER: US/10/790,396
/ PRIOR FILING DATE: 2004-03-01
/ PRIOR APPLICATION NUMBER: US/09/646,561
/ PRIOR FILING DATE: 2000-09-19
/ PRIOR APPLICATION NUMBER: 60/078,765
/ PRIOR FILING DATE: 1998-03-19
/ PRIOR APPLICATION NUMBER: 09/062,597
/ PRIOR FILING DATE: 1998-04-17
/ NUMBER OF SEQ ID NOS: 65
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 26
/ LENGTH: 332
/ TYPE: PRT
/ ORGANISM: Felis catus
US-10-790-396-26

Query Match          93.6%; Score 44; DB 16; Length 332;
Best Local Similarity 88.9%; Pred. No. 3.1;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GLVPIHOMS 9
Db      120 GLVPIHOMS 128

RESULT 4
US-10-790-396-17
/ Sequence 17, Application US/10790396
/ Publication No. US20040157296A1
/ GENERAL INFORMATION:
/ APPLICANT: Sim, Gek-Kee
/ APPLICANT: Yang, Shumin
/ APPLICANT: Sellins, Karen S.
/ TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY PROTEINS, NUCLEIC
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/ TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
/ FILE REFERENCE: IM-1-CI-PCT
/ CURRENT APPLICATION NUMBER: US/10/790,396
/ PRIOR FILING DATE: 2004-03-01
/ PRIOR APPLICATION NUMBER: US/09/646,561
/ PRIOR FILING DATE: 2000-09-19
/ PRIOR APPLICATION NUMBER: 60/078,765
/ PRIOR FILING DATE: 1998-03-19
/ PRIOR APPLICATION NUMBER: 09/062,597
/ PRIOR FILING DATE: 1998-04-17
/ NUMBER OF SEQ ID NOS: 65
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 17
/ LENGTH: 280
/ TYPE: PRT
/ ORGANISM: Canis familiaris
US-10-790-396-17

Query Match          87.2%; Score 41; DB 16; Length 280;
Best Local Similarity 77.8%; Pred. No. 9.8;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GLVPIHOMS 9
Db      119 GLVPIHOMS 127

RESULT 5
US-10-790-396-7
/ Sequence 7, Application US/10790396
/ Publication No. US20040157296A1
/ GENERAL INFORMATION:
/ APPLICANT: Sim, Gek-Kee
/ APPLICANT: Yang, Shumin
/ TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY PROTEINS, NUCLEIC
/ FILE REFERENCE: IM-1-CI-PCT
/ CURRENT APPLICATION NUMBER: US/10/790,396
/ PRIOR FILING DATE: 2004-03-01
/ PRIOR APPLICATION NUMBER: US/09/646,561
/ PRIOR FILING DATE: 2000-09-19
/ PRIOR APPLICATION NUMBER: 60/078,765
/ PRIOR FILING DATE: 1998-03-19
/ PRIOR APPLICATION NUMBER: 09/062,597
/ PRIOR FILING DATE: 1998-04-17
/ NUMBER OF SEQ ID NOS: 65
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 7
/ LENGTH: 329
/ TYPE: PRT
/ ORGANISM: Canis familiaris
US-10-790-396-7

Query Match          87.2%; Score 41; DB 16; Length 329;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GLVPIHOMS 9
Db      119 GLVPIHOMS 127

RESULT 6
US-10-425-115-208294
/ Sequence 208294, Application US/10425115
/ Publication No. US20040214272A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovacic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
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FILE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 208294
LENGTH: 96
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MWT4577_121557C.1.pap
US-10-425-115-208294

Query Match 78.7%; Score 37; DB 17; Length 96;
Best Local Similarity 85.7%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLVPIHQS 7
Db 78 GLVPIHQS 84

RESULT 7
US-10-389-647-604
Sequence 604, Application US/10389647
Publication No. US2004003549A1
GENERAL INFORMATION:
APPLICANT: GREENBERG, E. Peter
APPLICANT: SCHUSTER, Martin
APPLICANT: LOSTROH, Candis
TITLE OF INVENTION: QUORUM SENSING SIGNALING IN BACTERIA
FILE REFERENCE: UTZ-038CP
CURRENT APPLICATION NUMBER: US/10/389,647
CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 09/653730
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/153022
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 710
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 604
LENGTH: 99
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-10-389-647-604

Query Match 78.7%; Score 37; DB 15; Length 99;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLVPIHQS 9
Db 57 GLVPIHQS 65

RESULT 8
US-10-425-115-321220
Sequence 321220, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 321220
LENGTH: 122
TYPE: PRT

ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1) ..(122)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: MWT4577_56018C.1.pap
US-10-425-115-321220

Query Match 76.6%; Score 36; DB 17; Length 122;
Best Local Similarity 75.0%; Pred. No. 38;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LVPIHQS 9
Db 57 LVPIHQS 64

RESULT 9
US-10-282-122A-60956
Sequence 60956, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haasbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 60956
LENGTH: 261
TYPE: PRT
ORGANISM: Listeria monocytogenes
US-10-282-122A-60956

Query Match 76.6%; Score 36; DB 15; Length 261;
Best Local Similarity 66.7%; Pred. No. 85;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLVPIHQS 9

Db 238 GICPIHRMS 246

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1 RESULT 10
2 US-10-739-930-7964
3 : Sequence 7964, Application US/10739930
4 : Publication No. US20040216190A1
5 :
6 : GENERAL INFORMATION:
7 :
8 : APPLICANT: Kovalic, David K.
9 : TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
10 : TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
11 : FILE REFERENCE: 38-21(53377) B
12 : CURRENT APPLICATION NUMBER: US/10/739,930
13 : CURRENT FILING DATE: 2003-12-18
14 :
15 : NUMBER OF SEQ ID NOS: 11088
16 :
17 : SEQ ID NO 7964
18 :
19 : LENGTH: 317
20 :
21 : TYPE: PRT
22 :
23 : ORGANISM: Zea mays
24 :
25 : FEATURE:
26 :
27 : OTHER INFORMATION: Clone ID: ZEAHA-23APR03-C33206_3.p
28 :
29 : US-10-739-930-7964

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Query Match	74.5%	Score 35;	DB 17;	Length 317;
Best Local Similarity	55.6%	Pred. No. 1.6e+02;		
Matches	3;	Conservative	3;	Mismatches 1;
				Indels 0;
				Gaps 0;

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QY      1 GLVPIHQMS 9
         |||:::
Db      34 GLTPHQLT 42
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RESULT 11
US-09-864-761-42375
Sequence 42375, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30

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1      PRIOR APPLICATION NUMBER: PCT/US01/00661
2      PRIOR FILING DATE: 2001-01-30
3      PRIOR APPLICATION NUMBER: PCT/US01/00670
4      PRIOR FILING DATE: 2001-01-30
5      PRIOR APPLICATION NUMBER: US 60/234,687
6      PRIOR FILING DATE: 2000-09-21
7      PRIOR APPLICATION NUMBER: US 09/608,468
8      PRIOR FILING DATE: 2000-06-30
9      PRIOR APPLICATION NUMBER: US 09/774,203
10     PRIOR FILING DATE: 2001-01-29
11     NUMBER OF SEQ ID NOS: 49117
12     SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
13     SEQ ID NO 42375
14     LENGTH: 38
15     TYPE: PRT
16     ORGANISM: Homo sapiens
17     FEATURE:
18     OTHER INFORMATION: MAP TO A138734.2
19     OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.9
20     OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.3
21     OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.1
22     OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.4
23     OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.8
24     OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.3
25     OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.1
26     OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.3
27     OTHER INFORMATION: EST_HUMAN HIT: AA93362.1, EVALU6 2.00e-13
28     US-09-864-761.4-2375

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Query Match	72.3%	Score 34;	DB 9;	Length 38;
Best Local Similarity	85.7%	Pred. No. 27;		
Matches	6;	Conservative	0;	Mismatches 1; Indels 0; Gaps 0.

QY	1	GLVPIHQ	7
Db	15	GLTPIHQ	21

```

RESULT 12
US-10-425-115-212035
: Sequence 212035, Application US/10425115
: Publication No. US20040214272A1
: GENERAL INFORMATION:
: APPLICANT: La Rosa, Thomas J.
: APPLICANT: Kovalic, David K.
: APPLICANT: Zhou, Yihua
: APPLICANT: Cao, Yongswai
: TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
: TITLE OF INVENTION: Plants
: FILE REFERENCE: 38-21(5322)B
: CURRENT APPLICATION NUMBER: US/10/425,115
: CURRENT FILING DATE: 2003-04-28
: NUMBER OF SEQ. ID NOS: 369326
: SEQ ID NO 212035
: LENGTH: 89
: TYPE: PRT
: ORGANISM: Zea mays
: FEATURE:
: NAME/KEY: unsure
: LOCATION: (1)..(89)
: OTHER INFORMATION: unsure at all Xaa locations
: FEATURE:
: OTHER INFORMATION: Clone ID: MWT457_124578C.1.pep
US-10-425-115-212035

Query Match          72.3%;   Score 34;   DB 17;   Length 89;
Best Local Similarity 85.7%;   Pred.No. 67;
Matches      6;   Conservative      0;   Mismatches      1;   Indels      0;   Gaps      0;

Cy      1  GLVPIHQ 7
db      23  GLVPIHQ 29

```

```

Query Match 72.3% Score 34; DB 17; Length 89;
Best Local Similarity 85.7% Pred. No. 67;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0
QY 1 GLVPIHQ 7
Db 23 GLVPIHQ 29

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QY	1	GLVPITHQ	7
D5	23	GLVPETHQ	29

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RESULT 13
US-09-935-338-233
; Sequence 233, Application US/09935338
; Publication No. US20030073081A1
; GENERAL INFORMATION:
; APPLICANT: MIYAKI, Hiroyuki
; APPLICANT: SAGAWA, Hiroyuki
; APPLICANT: UEMORI, Takashi
; APPLICANT: YAMAMOTO, Junko
; APPLICANT: TOMONO, Jun
; APPLICANT: KOBAYASHI, Ei-ji
; APPLICANT: ENOKI, Tatsuji
; APPLICANT: TAKEDA, Osamu
; APPLICANT: MIYAKE, Kazuo
; APPLICANT: SATO, Yoshiaki
; APPLICANT: MORIYAMA, Mariko
; APPLICANT: SAWARAGI, Haruhisa
; APPLICANT: HAGIYA, Michio
; APPLICANT: ASADA, Kiyozo
; APPLICANT: KATO, Ikunoshin
; TITLE OF INVENTION: A method for amplification of nucleic acids
; FILE REFERENCE: MIYAKI-1
; CURRENT APPLICATION NUMBER: US/09/935,338
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: JP11-076966
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: JP11-370035
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: JP2000-251981
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: JP2000-284419
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: JP2000-288750
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: JP2001-104191
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: PCT/JP00/01534
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 233
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Thermotoga maritima
US-09-935-338-233

Query Match      72.3%; Score 34; DB 10; Length 238;
Best Local Similarity 55.6%; Pred. No. 1.9e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 GLVPIHQMS 9
DB      176 GVLPIHRLS 184

RESULT 14
US-10-380-430-59
; Sequence 59, Application US/10380430
; Publication No. US20040038366A1
; GENERAL INFORMATION:
; APPLICANT: UEMORI, Takashi
; APPLICANT: SATO, Yoshiaki
; APPLICANT: KOYAMA, No. US20040038366A1
; APPLICANT: HIRANO, Ryo
; APPLICANT: TAKAKURA, Hiakaru
; APPLICANT: KOBORI, Hirosaki
; APPLICANT: HASHIMOTO, Yuji
; APPLICANT: ASADA, Kiyozo
; APPLICANT: KATO, Ikunoshin
; TITLE OF INVENTION: THERMOTOLERANT RIBONUCLEASE H
; FILE REFERENCE: UEMORI-1
; CURRENT APPLICATION NUMBER: US/10/380,430
```

```
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: JP 2000-280785
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: JP 2001-064074
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT/JP01/07930
; PRIOR FILING DATE: 2001-09-13
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 59
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Thermotoga maritima
US-10-380-430-59

Query Match      72.3%; Score 34; DB 15; Length 238;
Best Local Similarity 55.6%; Pred. No. 1.9e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 GLVPIHQMS 9
DB      176 GVLPIHRLS 184

RESULT 15
US-10-282-122A-51529
; Sequence 51529, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA-034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,911
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51529
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Clostridium acetobutylicum
US-10-282-122A-51529
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Query Match 72.3%; Score 34; DB 15; Length 254;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GLVPIHQMS 9
| | | | |
| | | | |
Db 240 GTTPIHRMS 248

Search completed: December 15, 2004, 16:54:13
Job time : 89.4286 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 15, 2004, 16:28:26 ; Search time 10.7143 Seconds
(without alignments)
80.822 Million cell updates/sec

Title: US-09-868-605-14_COPY_113_121
Perfect score: 47
Sequence: 1 GLVPIHOMS 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:***
1: p1r1:***
2: p1r2:***
3: p1r3:***
4: p1r4:***

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match Length	DB ID	Description
1	38	80.9	330	146691	CD86 precursor - r
2	37	78.7	99	B83129	hypothetical prote
3	36	76.6	261	A11233	ribonuclease H rnh
4	35	74.5	434	S55579	D-nopaline dehydro
5	35	74.5	472	A13329	D-nopaline dehydro
6	35	74.5	1493	AC2555	hypothetical prote
7	34	72.3	228	B72320	ribonuclease H11
8	34	72.3	254	B97117	ribonuclease H11
9	34	72.3	263	A81446	acyl-[acyl-carrier
10	34	72.3	947	H85088	hypothetical prote
11	34	72.3	1353	JC4279	adenylate cyclase
12	33	70.2	159	F83710	hypothetical prote
13	33	70.2	261	AG1596	ribonuclease H rnh
14	33	70.2	278	FS1324	proteolipid protei
15	33	70.2	405	B69200	hypothetical prote
16	33	70.2	407	E87556	acyl-CoA dehydroge
17	33	70.2	411	D75408	phosphoglycerate k
18	33	70.2	453	AH0827	probable prs syste
19	33	70.2	586	D84710	hypothetical prote
20	33	70.2	728	A82352	iron(III) compound
21	33	70.2	2018	T34274	hypothetical prote
22	32	68.1	105	F84609	probable cysteine
23	32	68.1	109	I40396	flagellar protein
24	32	68.1	134	AE3490	hiti protein (impo
25	32	68.1	275	JC7604	CD86 spliced varia
26	32	68.1	329	A48754	B7-2 antigen - hum
27	32	68.1	345	T12350	NADH2 dehydrogenas
28	32	68.1	370	F86236	protein F14N23.9 l
29	32	68.1	391	D89526	30S ribosomal prot

ALIGNMENTS

30	32	68.1	402	2	F96640	hypothetical prote
31	32	68.1	430	2	B86805	hypothetical prote
32	32	68.1	450	2	T15154	hypothetical prote
33	32	68.1	476	2	T23232	hypothetical prote
34	32	68.1	481	2	D83466	probable two-compo
35	32	68.1	622	2	T23804	hypothetical prote
36	32	68.1	653	2	T51895	hypothetical prote
37	32	68.1	741	2	US0606	homeobox protein A
38	32	68.1	747	2	AG3031	conserved hypothet
39	32	68.1	747	2	D98254	hypothetical prote
40	32	68.1	872	2	JH0561	metabotropic gluta
41	32	68.1	978	2	H86319	hypothetical prote
42	32	68.1	1044	2	B72338	galactosyltransfer
43	32	68.1	3600	2	D86161	F1003.12 protein -
44	31	66.0	80	2	JT0435	hypothetical prote
45	31	66.0	80	2	T03187	hypothetical prote

RESULT 1

146691
CD86 precursor - rabbit
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004
C/Accession: 146691
R/Isono, T.; Seto, A.
Immunogenetics 42, 217-220, 1995
A/Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecu
A/Reference number: 146691
A/Status: preliminary; translated from GB/EMBL/DD3J
A/Molecule type: mRNA
A/Residues: 1-330 <ISO>
A/Cross-references: UNIPROT:P42071; GB:D49842; NID:G755098; PIDN:BA08642.1; PID:G75509;
C/Superfamily: B7-2 antigen

Query Match

Best Local Similarity 77.8%; Score 38; DB 2; Length 330;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLVPIHOMS 9

DB 119 GLVPIHOMN 127

RESULT 2

B83129
hypothetical protein PA4139 (imported) - Pseudomonas aeruginosa (strain PA01)
C/Species: Pseudomonas aeruginosa
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C/Accession: B83129

R/Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim
; Levy, S.; Olson, M.V.
Nature 406, 959-964, 2000

A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path
A/Reference number: A82950; MUID:20437337; PMID:10584043

A/Accession: B83129

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-99 <STO>
A/Cross-references: UNIPROT:Q9HWP2; GB:AE004830; GB:AE004091; NID:G950337; PIDN:AA0675;
C/Experimental source: strain PA01

C/Genetics: PA4139

Query Match

Best Local Similarity 78.7%; Score 37; DB 2; Length 99;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLVPIHOMS 9

Db 57 GLVPIHQMS 65

RESULT 3

ribonuclease H rnh homolog rnhB [imported] - *Listeria monocytogenes* (strain EGD-e)

C/Species: *Listeria monocytogenes*

C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C/Accession: A11233

A/Authors: P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussarguet, O.; Entian, K.D.; Fath, H.; Jones, L.M.; Karet, U.

Science 294, 849-852, 2001

A/Authors: Kretz, U.; Kuhn, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schueller, T.; Simoes, N.; Tietze, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A./Title: Comparative genomics of *Listeria* species.

A/Reference number: AB1077; MUID:21537279; PMID:11679669

C/Accession: A11233

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-261 <GLA>

A/Cross-references: UNIPROT:O8Y7K4; GB:NC_003210; PIDN:CAC99351.1; PID:G16410689; GSPDB:

C/Genetics:

C/Experimental source: strain EGD-e

C/Suprafamily: ribonuclease HII

Query Match

Best Local Similarity 76.6%; Score 36; DB 2; Length 261;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLVPIHQMS 9

Db 238 GLVPIHQMS 246

RESULT 4

D-nopaline dehydrogenase (EC 1.5.1.19) Noxa - *Agrobacterium tumefaciens*

C/Species: *Agrobacterium tumefaciens*

C/Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004

C/Accession: S55579

R/Zanker, H.; Lutz, G.; Langridge, U.; Langridge, P.; Schroeder, J.

submitted to the EMBL Data Library, February 1994

A/Description: Octopine and nopaline oxidases from Ti plasmids of *Agrobacterium tumefaciens*

A/Reference number: S55579

C/Accession: S55579

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-434 <ZAN>

A/Cross-references: UNIPROT:Q59158; EMBL:Z30316; NID:G496533; PIDN:CAA82963.1; PID:G49653

C/Keywords: oxidoreductase

Query Match

Best Local Similarity 74.5%; Score 35; DB 2; Length 434;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLVPIHQMS 9

Db 262 GLVPIHQMS 270

RESULT 5

D-nopaline dehydrogenase noxa [imported] - *Agrobacterium tumefaciens* (strain C58, Dupont)

C/Species: *Agrobacterium tumefaciens*

C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004

C/Accession: A13228

R/Wood, D.W.; Setuval, J.C.; Xaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Wood, I. et al.; Gillet, W.; Grant, C.; Guenther, D.; Kulyavin, T.; Levy, R.; Li, M.; McClellan, Science 294, 2317-2323, 2001

A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, B.W.

A/Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.

A/Reference number: AB2577; MUID:21608550; PMID:11743193

C/Accession: A13229

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-472 <KUR>

A/Cross-references: UNIPROT:O8U699; GB:AE008690; PIDN:AAL46255.1; PID:G17744034; GSPDB:

A/Experimental source: strain C58 (Dupont)

C/Genetics:

A/Genome: noxa

A/Genome: plasmid

Query Match

Best Local Similarity 74.5%; Score 35; DB 2; Length 472;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLVPIHQMS 9

Db 262 GLVPIHQMS 270

RESULT 6

hypothetical protein alr8034 [imported] - *Nostoc* sp. (strain PCC 7120) plasmid pCC7120g

C/Species: *Nostoc* sp. PCC 7120

A/Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120

C/Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C/Accession: AC2555

R/Xaneho, T.; Nakamura, Y.; Wolk, C.P.; Kurlitz, T.; Sasamoto, S.; Watanabe, A.; Iriyuch Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takasawa, M.; Yamada, M.; Tabata, DNA Res. 8, 205-213, 2001

A/Title: Complete genomic sequence of the filamentous nitrogen-fixing *Cyanobacterium* An

A/Reference number: AB1807; MUID:21595285; PMID:11759840

C/Accession: AC2555

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1499 <KUR>

A/Cross-references: UNIPROT:O8YK83; GB:AP003603; PIDN:BAW7364.1; PID:G17134807; GSPDB:

C/Genetics:

A/Genome: plasmid

Query Match

Best Local Similarity 74.5%; Score 35; DB 2; Length 1499;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 LVPIHQMS 9

Db 1389 LVPIHQMS 1396

RESULT 7

ribonuclease HII - *Thermotoga maritima* (strain MSB8)

C/Species: *Thermotoga maritima*

C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C/Accession: B72320

R/Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hicke Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D. C.M.

Nature 399, 323-329, 1999

A/Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se

A/Reference number: A72200; MUID:99287316; PMID:10360571

C/Accession: B72320

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-238 <ARN>

A/Cross-references: UNIPROT:O9X017; GB:AE001755; GB:AE000512; NID:G4981432; PIDN:AAD359

A/Experimental source: strain MSB8

C/Genetics:

A:Gene: TW0915
C:Superfamily: ribonuclease HII
Query Match 72.3%; Score 34; DB 2; Length 238;
Best Local Similarity 55.6%; Pred. No. 24;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
Db 176 GVPIHQMS 164

RESULT 8
E97117
ribonuclease HII [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C:Accession: E97117
R:Rolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A>Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld
A:Reference number: A96900; MIMD:21359325; PMID:21359325
A:Accession: E97117
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-254 <KUR>
A:Cross-references: UNIPROT:Q97190; GB:AE001437; PIDN:AAK79728.1; PID:g15024732; GSPDB:C
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC1762

Query Match 72.3%; Score 34; DB 2; Length 254;
Best Local Similarity 66.7%; Pred. No. 26;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Db 240 GTPIHQMS 248

RESULT 9
A81446
acyl-l-acyl-carrier-protein [UDP-N-acetylglucosamine O-acyltransferase (EC 2.3.1.129) C]O
C:Species: Campylobacter jejuni
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: A81446
R:Parikh, J.; Wren, B.W.; Mungall, K.; Kettle, J.M.; Churcher, C.; Basham, D.; Chilling, C.W.; Quail, M.; Raftery, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrel, Nature 403, 665-668, 2000
A>Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyf
A:Reference number: A81250; MIMD:20150912; PMID:10688204
A:Accession: A81446
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-263 <PBR>
A:Cross-references: UNIPROT:Q9PIM1; GB:AL139074; GB:AL111168; NID:g6967505; PIDN:CAB7274
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: lpxA; Cj0274
C:Superfamily: acyl-l-acyl-carrier-protein [UDP-N-acetylglucosamine O-acyltransferase
C:Keywords: acyltransferase

Query Match 72.3%; Score 34; DB 2; Length 263;
Best Local Similarity 85.7%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 152 GLVPIHQ 158

RESULT 10

H85088
hypothetical protein AT4G08830 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: H85088
R:Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Nature 402, 769-777, 1999
A>Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MIMD:20083488; PMID:10617198
A:Accession: H85088
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-947 <STO>
A:Cross-references: UNIPROT:Q9JDL8; GB:NC_001268; NID:g7267526; PIDN:CAB78008.1; GSPDB:C
C:Genetics:
A:Gene: AT4G08830
A:Map position: 4

Query Match 72.3%; Score 34; DB 2; Length 947;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Db 476 LIPPIHQMS 483

RESULT 11
JC4279
adenylate cyclase (EC 4.6.1.1) type 10 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C:Accession: JC4279
R:Paterson, J.M.; Smith, S.W.; Hartmar, A.U.; Antoni, F.A.
Biochem. Biophys. Res. Commun. 214, 1000-1008, 1995
A>Title: Control of a novel adenylyl cyclase by calcineurin.
A:Reference number: JC4279; MIMD:96024597; PMID:7575502
A:Accession: JC4279
A:Molecule type: mRNA
A:Residues: 1-1353 <PAT>
A:Cross-references: UNIPROT:P51830; EMBL:Z50190
A:Experimental source: A1T20 cells
C:Comment: This enzyme is the target of regulation by calcineurin and is a physiological messenger molecules.

C:Superfamily: human adenylyl cyclase: guanylate cyclase catalytic domain homology
C:Keywords: phosphorus-oxygen lyase; transmembrane protein
F:118-137/Domain: transmembrane #status predicted <TM01>
F:142-163/Domain: transmembrane #status predicted <TM02>
F:173-193/Domain: transmembrane #status predicted <TM03>
F:230-241/Domain: transmembrane #status predicted <TM05>
F:244-264/Domain: transmembrane #status predicted <TM06>
F:284-304/Domain: transmembrane #status predicted <TM06>
F:313-375/Domain: guanylate cyclase catalytic domain homology <GCC>
F:787-807/Domain: transmembrane #status predicted <TM07>
F:819-839/Domain: transmembrane #status predicted <TM08>
F:865-885/Domain: transmembrane #status predicted <TM09>
F:891-911/Domain: transmembrane #status predicted <TM10>
F:921-941/Domain: transmembrane #status predicted <TM11>
F:977-997/Domain: transmembrane #status predicted <TM12>
F:1051-1246/Domain: guanylate cyclase catalytic domain homology <GCC2>

Query Match 72.3%; Score 34; DB 2; Length 1353;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Db 1249 GVPIHQMS 1257

RESULT 12
P83710
hypothetical protein BH0486 [imported] - Bacillus halodurans (strain C-125)

C/Species: *Bacillus halodurans*
 C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
 C/Accession: F83710
 R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Saeki, R.; Masui, N.; Fuji, F.; Hira
 Molecule Acids Res. 28, 4317-4331, 2000
 A/Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
 A/Reference number: A83650; MUID:20512582; PMID:11058132
 A/Accession: F83710
 A/Status: Preliminary
 A/Molecule type: DNA
 A/Residues: 1-159 <STO>
 A/Cross-references: UNIPROT:Q9KRU3; GB:AP001508; GB:BA000004; NID:g10172890; PIDN:BA042
 A/Experimental source: strain C-125
 C/Genetics:
 A/Gene: BH046
 C/Superfamily: *Bacillus subtilis* hypothetical protein ytes

Query Match
 Best Local Similarity 70.2%; Score 33; DB 2; Length 159;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLVPIHOMS 9
 DB 88 GLVPIHOMS 96

RESULT 13
 AG156
 ribonuclease H rnh homolog rnhB [imported] - *Listeria innocua* (strain C1p11262)
 C/Species: *Listeria innocua*
 C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
 C/Accession: AG1596
 R/Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
 D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
 Science 294, 849-852, 2001
 A/Authors: Krett, J.; Kuhn, M.; Kunst, F.; Kurapkac, G.; Macheno, E.; Maitournam, A.; Ma
 ok, C.; Schlueter, T.; Simoes, N.; Tietzer, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland,
 A/Title: Comparative genomics of *Listeria* species.
 A/Reference number: AB1077; MUID:21537279; PMID:11679669
 A/Accession: AG1596
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-261 <GLA>
 A/Cross-references: UNIPROT:Q92C79; GB:AL592022; PIDN:CAC96543.1; PID:G16413785; GSPDB:G
 A/Experimental source: strain C1p11262
 C/Genetics:
 A/Gene: rnhB
 C/Superfamily: ribonuclease HII

Query Match
 Best Local Similarity 70.2%; Score 33; DB 2; Length 261;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLVPIHOMS 9
 DB 238 GLVPIHOMS 246

RESULT 14
 I51324
 proteolipid protein DM beta - spiny dogfish
 C/Species: *Squalus acanthias* (spiny dogfish)
 C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
 C/Accession: I51324
 R/Kitagawa, K.; Sinoway, M.P.; Yang, C.; Gould, R.M.; Colman, D.R.
 Neuron 11, 433-448, 1993
 A/Title: A proteolipid protein gene family: expression in sharks and rays and possible e
 A/Reference number: I51323; MUID:94000610; PMID:8338138
 A/Accession: I51324
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-278 <KIT>

A/Cross-references: UNIPROT:P36644; EMBL:U02974; NID:g409971; PIDN:AA059640.1; PID:g409
 C/Superfamily: myelin proteolipid protein

Query Match
 Best Local Similarity 70.2%; Score 33; DB 2; Length 278;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLVPIHQ 7
 DB 181 GLVPIHQ 187

RESULT 15
 B69200
 hypothetical protein MTH749 - *Methanobacterium thermoautotrophicum* (strain Delta H)
 C/Species: *Methanobacterium thermoautotrophicum*
 C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
 C/Accession: B69200
 R/Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, D.; Aldredge, T.;
 Ki, S.; Church, G.M.; Daniels, C.O.; Mao, J.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
 U. Bacteriol. 179, 7135-7155, 1997
 A/Title: Complete genome sequence of *Methanobacterium thermoautotrophicum* Delta H: funct
 A/Reference number: A69000; MUID:98037514; PMID:9371463
 A/Accession: B69200
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-405 <MTH>
 A/Cross-references: UNIPROT:Q26844; GB:AE000853; GB:AE000666; NID:g2621824; PIDN:AA052525
 A/Experimental source: strain Delta H
 C/Genetics:
 A/Gene: MTH749

Query Match
 Best Local Similarity 70.2%; Score 33; DB 2; Length 405;
 Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLVPIHOMS 9
 DB 69 GLVPIHOMS 77

Search completed: December 15, 2004, 16:38:00
 Job time: 13.7143 secs

GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: December 15, 2004, 16:24:31, Search time 49.7143 Seconds
(without alignments)
104.163 Million cell updates/sec

Title: US-09-868-605-14_COPY_113_121

Perfect score: 47

Sequence: 1 GLVPIHOMS 9

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: 1: UniProt_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	325	2	C02838
2	44	93.6	329	2	Q9XSX6
3	44	93.6	332	2	Q9GM27
4	44	93.6	332	2	Q9SL16
5	41	87.2	280	2	Q9TTF1
6	41	87.2	329	2	Q9TTF2
7	39	83.0	284	2	Q9GLJ3
8	38	80.9	330	1	CD86_RABBIT
9	38	80.9	412	2	Q89E49
10	37	78.7	99	2	Q9HWP2
11	37	78.7	378	2	Q7MD30
12	37	78.7	378	2	Q8D611
13	37	78.7	812	2	Q7UFI1
14	36	76.6	90	2	Q84DX1
15	36	76.6	126	2	Q89Y03
16	36	76.6	251	2	Q881X8
17	36	76.6	261	1	RNH2_LISMO
18	36	76.6	411	2	Q6NL37
19	36	76.6	411	2	Q810H8
20	36	76.6	411	2	AAS93776
21	36	76.6	1081	2	Q7UHS1
22	36	76.6	6858	2	Q7QUM1
23	35	74.5	257	1	LPXA_FUSNN
24	35	74.5	257	2	Q7P452
25	35	74.5	314	2	Q7X9W7
26	35	74.5	425	1	Y4RF_RHISN
27	35	74.5	434	2	Q59158
28	35	74.5	472	2	Q7D208
29	35	74.5	472	2	Q9R691
30	35	74.5	472	2	Q8U699
31	35	74.5	1323	2	Q8SV50

32	35	74.5	1334	1	CYA9_CHICK	Q9dgg6 gallus gall
33	35	74.5	1499	2	Q8YK63	Q8YK63 anabaena sp
34	34	72.3	226	2	Q7NNB8	Q7nnb8 gloebacter
35	34	72.3	238	1	RNH2_THEMA	Q9x017 thermotoga
36	34	72.3	249	1	ABG1_LACTIC	Q48725 lactococcus
37	34	72.3	250	2	Q8DSH5	Q8dsh5 streptococc
38	34	72.3	254	1	RNH2_CLOAB	Q97190 clostridium
39	34	72.3	263	1	LPXA_CAMDE	Q9p1n1 campylobact
40	34	72.3	281	2	P94301	P94301 bacillus fi
41	34	72.3	315	2	Q82CR7	Q82cr7 streptomyce
42	34	72.3	400	2	Q6M5E1	Q6m5e1 corynebacte
43	34	72.3	400	2	CAF21448	Ca121448 corynebac
44	34	72.3	479	2	Q7D066	Q72d66 desulfocvibr
45	34	72.3	479	2	AAS95543	Aas95543 desulfovibr

ALIGNMENTS

RESULT 1					
ID	C02838	PRELIMINARY:	PRT:	325 AA.	
AC	Q02838:				
DT	01-JUL-1997 (TREMBlrel. 04, Created)				
DT	01-JUL-1997 (TREMBlrel. 04, Last sequence update)				
DT	01-OCT-2003 (TREMBlrel. 25, Last annotation update)				
DE	B7-2.				
GN	Name=CD86:				
OS	Sus scrofa (pig).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.				
OX	NCBI_TaxID=9823;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=97047772; PubMed=8892613;				
RA	Maier S.E., Karmann K., Win W., Hughes C.C., Pober J.S.,				
RA	Bothwell A.L.;				
RT	"Porcine endothelial CD86 is a major costimulator of xenogeneic human				
RT	T cells: cloning, sequencing, and functional expression in human				
RT	endothelial cells";				
RU	J. Immunol. 157:3838-3944(1996).				
DR	EMBL: L76099; AAB61307.1; -.				
DR	HSSP; P42081; INCN.				
DR	InterPro; IPR007110; IG-like.				
DR	InterPro; IPR003596; IG_v.				
DR	Pfam; PF00047; IG_1.				
DR	SMART; SMO0406; IGV; 1.				
DR	PROSITE; PS50835; IG_LIKE; 1.				
SQ	SEQUENCE 325 AA, 36527 MW; 988BB08137B0597D CRC64;				
Query Match					
Best Local Similarity 100.0%; Score 47; DB 2; Length 325;					
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1	GLVPIHOMS 9			
DB	113	GLVPIHOMS 121			
RESULT 2					
ID	Q9XSX6	PRELIMINARY:	PRT:	329 AA.	
AC	Q9XSX6:				
DT	01-NOV-1999 (TREMBlrel. 12, Created)				
DT	01-NOV-1999 (TREMBlrel. 12, Last sequence update)				
DT	01-OCT-2003 (TREMBlrel. 25, Last annotation update)				
DE	CD86 anti-gen.				
GN	Name=CD86:				
OS	Felis silvestris catus (Cat).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.				
OX	NCBI_TaxID=9685;				
RN	[1]				

```

RP SEQUENCE FROM N.A.
RX MEDLINE=20180222; PubMed=10713336;
RA Choi I.S., Hash S.M., Winslow B.J., Collisson E.W.;
RT "Sequence analyses of feline B7 costimulatory molecules.";
RL Vet. Immunol. Immunopathol. 73:219-231(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Choi I.S., Hash S., Winslow B.J., Collisson E.W.;
RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF157827; AAD42974.1; -.
DR HSSP; P42081; INCN.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
SQ SEQUENCE 329 AA; 37481 MW; A10621E3C00A08BB CRC64;

Query Match
Best Local Similarity 93.6%; Score 44; DB 2; Length 329;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLVPHQMS 9
Db 120 GLVPHQMS 128

RESULT 3
O9GMZ7 PRELIMINARY; PRT; 332 AA.
ID O9GMZ7
AC O9GMZ7;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE B-lymphocyte activation antigen B7-2 (CD86).
GN Name=CD86;
OS Fells silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Fells.
OX NCBI_TaxId=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20485322; PubMed=11029611;
RX Nishimura Y., Shimojima M., Miyazawa T., Sato E., Nakamura K.,
RA Izumiya Y., Ikeda Y., Mikami T., Takahashi E.;
RT "Molecular cloning of the cDNA encoding the feline B-lymphocyte
RT activation antigen B7-1 (CD80) and B7-2 (CD86) homologues which
RT interact with human CTLA4-Ig.";
RL Eur. J. Immunogenet. 27:427-430(2000).
DR EMBL; AB030652; BAB11688.1; -.
DR HSSP; P42081; INCN.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
SQ SEQUENCE 332 AA; 37812 MW; 672C8B3667D1E3C0 CRC64;

Query Match
Best Local Similarity 93.6%; Score 44; DB 2; Length 332;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLVPHQMS 9
Db 120 GLVPHQMS 128

RESULT 4
O9SL16 PRELIMINARY; PRT; 332 AA.
ID O9SL16
AC O9SL16;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE CD8c.

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GN Name=CD86;
OS Fells silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Fells.
OX NCBI_TaxId=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21390213; PubMed=11498243;
RX Yang S., Sellins K.S., Powell T., Storeran E., Sim G.K.;
RT "Novel transcripts encoding secreted forms of feline CD80 and CD86
RT costimulatory molecules.";
RL Vet. Immunol. Immunopathol. 81:15-21(2001).
DR EMBL; AY007704; AAG23342.1; -.
DR HSSP; P42081; INCN.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
SQ SEQUENCE 332 AA; 37826 MW; 8BFC8B3667D1E3D8 CRC64;

Query Match
Best Local Similarity 93.6%; Score 44; DB 2; Length 332;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLVPHQMS 9
Db 120 GLVPHQMS 128

RESULT 5
O9TFP1 PRELIMINARY; PRT; 280 AA.
ID O9TFP1
AC O9TFP1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2004 (TREMBLrel. 26, Last annotation update)
DE Truncated B7-2 protein.
GN Name=CD86;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxId=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20093986; PubMed=10630300;
RX Yang S., Sim G.-K.;
RT "New forms of dog CD80 and CD86 transcripts that encode secreted B7
RT molecules.";
RL Immunogenetics 50:349-353(1999).
DR EMBL; AF106827; AAF17298.1; -.
DR HSSP; P42081; INCN.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 280 AA; 32255 MW; 3C8EBCA4D826A7F3 CRC64;

Query Match
Best Local Similarity 87.2%; Score 41; DB 2; Length 280;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLVPHQMS 9
Db 119 GLVPHQMS 127

RESULT 6
O9TFP2 PRELIMINARY; PRT; 329 AA.
ID O9TFP2
AC O9TFP2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)

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DT 01-MAY-2000 (TEMBLrel. 13, last sequence update)
DE 01-MAR-2004 (TEMBLrel. 26, last annotation update)
DB B7-2 protein.
OS Name=CD86;
OC Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20039396; PubMed=10630300;
RA Yang S., Sim G.-K.;
RT "New forms of dog CD80 and CD86 transcripts that encode secreted B7
  molecules."
RL Immunogenetics 50:349-353(1999).
DR EMBL; AF106826; AAF17297.1; -.
DR HSSP; P42081; INCN.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 329 AA; 37774 MW; D98BB63437BF7B73 CRC64;

Query Match      87.2%; Score 41; DB 2; Length 329;
Best Local Similarity 77.8%; Pred. No. 8.8;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLVPIHOMS 9
DB 119 GLVPIHOMS 127

RESULT 7
Q9GLJ3 PRELIMINARY; PRT; 284 AA.
AC Q9GLJ3;
DT 01-MAR-2001 (TEMBLrel. 16, Created)
DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE C86 antigen (Fragment).
GN Name=CD86;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Peripheral blood;
RA Brooke G.P., Howard C.J., Parsons K.R.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL291475; CAC13140.1; -.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_v.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IGV; 1.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON TER 284
SQ SEQUENCE 284 AA; 32021 MW; 797BB639E297841 CRC64;

Query Match      83.0%; Score 39; DB 2; Length 284;
Best Local Similarity 88.9%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLVPIHOMS 9
DB 126 GLVPIHOMS 134

RESULT 8
CD86_RABBIT

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ID CD86_RABBIT STANDARD; PRT; 330 AA.
AC P42071;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE B lymphocyte activation antigen CD86 precursor (Activation B7-2
  antigen)
GN Name=CD86;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=B/T X CHB; HM;
RX MEDLINE=95369849; PubMed=7642234;
RA Iseno T., Seto A.;
RT "Cloning and sequencing of the rabbit gene encoding T-cell
  costimulatory molecules."
RL Immunogenetics 42:217-220(1995).
CC -!- FUNCTION: Receptor involved in the costimulatory signal essential
  for T lymphocyte proliferation and interleukin 2 production, by
  binding CD28 or CTLA-4. May play a critical role in the early
  events of T cell activation and costimulation of native T cells,
  such as deciding between immunity and anergy that is made by T
  cells within 24 hours after activation.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D49842; BAA08642.1; -.
DR PIR; I46591; I46691.
DR HSSP; P42081; INCN.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Glycoprotein; Immunoglobulin domain; Receptor; Signal; T-cell;
  Transmembrane.
FT SIGNAL 1..22
FT CHAIN 23..330
FT DOMAIN 23..247
FT TRANSMEM 248..268
FT DOMAIN 269..330
FT DOMAIN 33..127
FT DOMAIN 150..225
FT DISULFID 40..110
FT DISULFID 157..218
FT CARBOHYD 33..33
FT CARBOHYD 135..135
FT CARBOHYD 146..146
FT CARBOHYD 154..154
FT CARBOHYD 177..177
FT CARBOHYD 192..192
FT CARBOHYD 198..198
FT CARBOHYD 213..213
SQ SEQUENCE 330 AA; 37142 MW; 935CD65C57B3EB1 CRC64;

Query Match      80.9%; Score 38; DB 1; Length 330;
Best Local Similarity 77.8%; Pred. No. 36;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLVPIHOMS 9

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Db 119 GLVPIYOMN 127

RESULT 9

089E49 PRELIMINARY; PRT; 412 AA.
AC 089E49;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DE 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE BL17238 protein.
GN OrderedlocusNames=bl17238;
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobiaceae;
OC NCBI_TaxId=375;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=USDA110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
RA Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
Bradyrhizobium japonicum USDA110."
RT DNA Res. 9:189-197(2002).
RL EMBL; AP005961; BAC52503.1; -
KW Complete proteome.
SQ SEQUENCE 412 AA; 43969 MW; B801F68836C8F7BE CRC64;

Query Match 80.9%; Score 38; DB 2; Length 412;
Best Local Similarity 66.7%; Pred. No. 45;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLVPIHOMS 9
Db 276 GLVPIHOMS 284

RESULT 10

09HWP2 PRELIMINARY; PRT; 99 AA.
AC 09HWP2;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedlocusNames=PA4139;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OC NCBI_TaxId=287;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Storer C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.V., Brinkman F.S.D., Hutnagle W.O., Kowalik D.V., Lagrou M.,
RA Gaeber R.L., Goltzy L., Tolentino E., Westbrook-Wedman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., West A., Labdig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reiter J., Sater M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
opportunistic pathogen."
RT Nature 406:959-964(2000).
RL EMBL; AE004830; AAC07526.1; -
DR PIR; B83129; B83129.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 99 AA; 10437 MW; 62706B205A63F966 CRC64;

Query Match 78.7%; Score 37; DB 2; Length 99;

Best Local Similarity 66.7%; Pred. No. 17;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLVPIHOMS 9
Db 57 GLVPIHOMS 65

RESULT 11

07MD30 PRELIMINARY; PRT; 378 AA.
AC 07MD30;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DE N-acetylglucosamine-6-phosphate deacetylase.
GN Name=VVA1206;
OS Vibrio vulnificus (strain V016).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
OC NCBI_TaxId=196600;
RN (1)
RP SEQUENCE FROM N.A.
RX PubMed=14656965;
RA Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
RA Liao T.-L., Liu Y.-M., Chen H.-Y., Shen A.B.-T., Li J.-C., Su T.-L.,
RA Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;
RT "Comparative genome analysis of Vibrio vulnificus, a marine
pathogen."
RT Genome Res. 13:2577-2587(2003).
RL EMBL; AP005349; BAC97233.1; -
DR GO; GO:0016787; Phosphatase activity; IEA.
DR GO; GO:0008448; N-acetylglucosamine-6-phosphate deacetylase; IEA.
DR GO; GO:0006044; N-acetylglucosamine metabolism; IEA.
DR InterPro; IPR006680; Amidohydro_1.
DR InterPro; IPR011550; Amidohydro_1.
DR InterPro; IPR003764; Naga.
DR Pfam; PF01979; Amidohydro_1; 1.
DR ProDom; PD001248; Amidohydro_1like; 1.
DR TrIRPfam; TIGR00221; naga; 1.
SQ SEQUENCE 378 AA; 41513 MW; C8B55701F5C2F5BD CRC64;

Query Match 78.7%; Score 37; DB 2; Length 378;
Best Local Similarity 77.8%; Pred. No. 66;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLVPIHOMS 9
Db 32 GLVPIHOMS 40

RESULT 12

08D611 PRELIMINARY; PRT; 378 AA.
AC 08D611;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE N-acetylglucosamine-6-phosphate deacetylase.
GN OrderedlocusNames=VV20736;
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
OC NCBI_TaxId=672;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=CMCP6;
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.T., Moon Y.H., Jeong H.,
RA Choe H.E.;
RT "Complete genome sequence of Vibrio vulnificus CMCP6."
RT Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF016810; AAC07668.1; -
DR GO; GO:0016787; Phosphatase activity; IEA.

DR GO: GO:0008448; F:N-acetylglucosamine-6-phosphate deacetylase. . .; IEA.
 DR GO: GO:0006044; F:N-acetylglucosamine metabolism; IEA.
 DR InterPro: IPR006680; Amidohydro_1.
 DR InterPro: IPR011550; Amidohydro_1.
 DR InterPro: IPR011059; Metallo_hydrolase.
 DR InterPro: IPR003764; Naga_hydrolyase.
 DR Pfam: PF01979; Amidohydro_1; 1.
 DR ProDom: PD001248; Amidohydro_1; 1.
 DR TrRfam: TRFR00221; naga; 1.
 KW Complete proteome.
 SQ SEQUENCE 378 AA; 41494 MW; 5084CDA042824B68 CRC64;

Query Match 78.7%; Score 37; DB 2; Length 378;
 Best Local Similarity 77.8%; Pred. No. 66;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLVPIHOMS 9
 DB 32 GLVPIHOMS 40

RESULT 13

Q7UIF1 PRELIMINARY; PRT; 812 AA.
 AC Q7UIF1;
 DT 01-OCT-2003 (TRENBLrel. 25, Created)
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Serine/threonine-protein kinase.
 GN OrderedLocustNames=RB12572;
 OS Rhodospirillum rubrum.
 OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
 OC Planctomycetaceae; Pirellula.
 OX NCBI_TaxID=117;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1;
 RX MEDLINE=22735913; PubMed=12835416;
 RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
 RA Ludwig W., Gade D., Beck K., Borzym K., Heilmann K., Rabus R.,
 RA Schlesner H., Aumann R., Reinhardt R.;
 RT "Complete genome sequence of the marine planctomycete Pirellula sp.
 strain 1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL: BX294155; CAD7663.1; -
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO: GO:0016740; F:transferase activity; IEA.
 DR InterPro: IPR006488; F:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR008271; Ser_thr_pkin_AS.
 DR Pfam: PF00069; Pkinase; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR ProSite: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Complete proteome; Kinase;
 KW Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 812 AA; 90937 MW; C812980D4358EAA CRC64;

Query Match 78.7%; Score 37; DB 2; Length 812;
 Best Local Similarity 62.5%; Pred. No. 1.4e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLVPIHOM 8
 DB 138 GLVPIHOM 145

RESULT 14
 Q84DX1 PRELIMINARY; PRT; 90 AA.

AC Q84DX1;
 DT 01-JUN-2003 (TRENBLrel. 24, Created)
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Possible VIV repeat protein.
 OS Tropheryma whipplei (Whipple's bacillus) (Tropheryma whippelii).
 OC Bacteria; Actinobacteria; Actinomycetidae; Actinomycetales;
 OC Micrococciaceae; Cellulomonadaceae; Tropheryma.
 OX NCBI_TaxID=2039;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22632143; PubMed=12747404;
 RA Matwald M., Lepp P.W., Reiman D.A.;
 RT "Analysis of conserved non-rRNA genes of Tropheryma whippelii.";
 RL Syst. Appl. Microbiol. 26:3-12(2003).
 DR EMBL: AF483650; AA084489.1; -
 SQ SEQUENCE 90 AA; 9885 MW; C1DC13F5A48B471 CRC64;

Query Match 76.6%; Score 36; DB 2; Length 90;
 Best Local Similarity 87.5%; Pred. No. 25;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LVPIHOMS 9
 DB 25 LVPIHOMS 32

RESULT 15

Q89Y03 PRELIMINARY; PRT; 126 AA.
 AC Q89Y03;
 DT 01-JUN-2003 (TRENBLrel. 24, Created)
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Cytochrome O ubiquinol oxidase subunit IV.
 GN Name=Cyod; OrderedLocustNames=bl010152;
 OS Bradyrhizobium japonicum.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Bradyrhizobium.
 OX NCBI_TaxID=375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=USDA110;
 RX MEDLINE=22484998; PubMed=12597275;
 RA Kurek T., Nakamura Y., Sato S., Minamisawa K., Uehimi T.,
 RA Sasamoto S., Watanabe A., Idegawa K., Iiguchi M., Kawashima K.,
 RA Kohara M., Matsunoto M., Shimo S., Tsuruoka H., Wada T., Yamada M.,
 RA Tabata S.;
 RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
 Bradyrhizobium japonicum USDA110.";
 RL DNA Res. 9:185-197(2002).
 DR EMBL: AP005935; BAC45417.1; -
 DR InterPro: IPR005171; COX4_pro.
 DR Pfam: PF03626; COX4_pro; 1.
 KW Complete proteome.
 SQ SEQUENCE 126 AA; 13951 MW; 919D87A5633BF1B3 CRC64;

Query Match 76.6%; Score 36; DB 2; Length 126;
 Best Local Similarity 75.0%; Pred. No. 35;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LVPIHOMS 9
 DB 116 LVPIHOMS 123

Search completed: December 15, 2004, 16:33:36
 Job time : 51.7143 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 15, 2004, 16:27:41 ; Search time 129.143 Seconds
(without alignments)
33.333 Million cell updates/sec

Title: US-09-868-605-14_COPY_151_162
Perfect score: 69
Sequence: 1 CSSTQGYPPQR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: A_Geneseq_23Sep04:*
2: geneseqp1980s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	69	100.0	29	3 AAY95330	Aay95330 OVA323-33
2	69	100.0	250	3 AAW14944	Aaw14944 Chimeric
3	69	100.0	325	3 AAY95321	Aay95321 Pig cost.
4	69	100.0	325	3 AAY95324	Aay95324 Human cos
5	54	78.3	280	2 AAY1076	Aay1076 Canine B7
6	54	78.3	329	2 AAY1076	Aay1076 Canine B7
7	54	78.3	329	3 AAY32278	Aay32278 Cat CD86
8	54	78.3	329	3 AAY32285	Aay32285 Feline CD
9	54	78.3	329	5 AAO17734	Aao17734 Feline CD
10	54	78.3	329	5 AAU78121	Aau78121 Feline CD
11	54	78.3	332	2 AAY41079	Aay41079 Feline B7
12	51	73.9	102	2 AAW08473	Aaw08473 Human B7
13	51	73.9	102	3 AAB37093	Aab37093 Human B7
14	51	73.9	244	2 AAW90209	Aaw90209 hb7, this
15	51	73.9	246	2 AAW86005	Aaw86005 Human B7
16	51	73.9	246	4 AAB83837	Aab83837 Amino aci
17	51	73.9	260	2 AAW42339	Aaw42339 CD86 extr
18	51	73.9	323	2 AAW71478	Aaw71478 B70 type
19	51	73.9	323	2 AAY44290	Aay44290 Human B7
20	51	73.9	323	5 AAE15830	Aae15830 Human co-
21	51	73.9	323	7 ADD25560	Add25560 Binding d
22	51	73.9	323	8 ADU54625	Adj54625 Human B7-
23	51	73.9	324	5 AAO15801	Aao15801 Human B7-
24	51	73.9	329	2 AAR67984	Aar67984 Human B1
25	51	73.9	329	2 AAW08467	Aaw08467 Human B1

26	51	73.9	329	2 AAW73638	Aaw73638 Human B7-
27	51	73.9	329	3 AAB37085	Aab37085 Human B1
28	51	73.9	329	5 AAB78364	Aab78364 Amino aci
29	51	73.9	329	5 AAE14634	Aae14634 Human B7-
30	51	73.9	329	7 ABW00432	Abw00432 Human CD2
31	51	73.9	329	7 ADD45302	Add45302 Human Pro
32	51	73.9	329	7 ADK59860	Adk59860 Human B7-
33	51	73.9	329	8 ADI19364	Adi19364 Human B7-
34	51	73.9	329	8 ADJ54626	Adj54626 Human B7-
35	51	73.9	329	8 ADP12511	Adp12511 Proteas e
36	51	73.9	477	2 AAW90207	Aaw90207 hb7, 2PC s
37	50	72.5	313	2 AAW34452	Aaw34452 Rat CD86
38	50	72.5	313	7 ADD45300	Add45300 Rat Prote
39	48	69.6	324	4 AAB48665	Aab48665 Human CD8
40	47	68.1	453	7 ADK68210	Adk68210 Novel NOV
41	46	66.7	216	4 AAB87417	Aab87417 Human gen
42	46	66.7	216	4 AAU00950	Aau00950 Human B7-
43	46	66.7	216	7 ADK68226	Adk68226 Novel NOV
44	46	66.7	244	4 AAU00949	Aau00949 Human B7-
45	46	66.7	315	5 AAE19141	Aae19141 Murine B7

ALIGNMENTS

RESULT 1	
ID	AAY95330 standard; peptide: 29 AA.
XX	XX
AC	AAY95330;
XX	XX
DT	12-SEP-2003 (revised)
DT	25-SEP-2000 (first entry)
XX	XX
DE	OVA323-339-pig costimulatory molecule B7-2 epitope hybrid peptide 6.
XX	XX
KW	Co-stimulatory molecule; CD86, B7-2; pig; immunosuppressive;
KW	xerotransplantation; organ transplan; vaccine; B-cell epitope;
KW	T-cell epitope; ovalbumin; chicken.
OS	Gallus sp.
OS	Sus scrofa.
OS	Chimeric.
XX	XX
FT	Key
FT	Peptide
FT	Location/Qualifiers
FT	1..17
FT	/note= "OVA323-339"
FT	18..29
FT	/note= "B7-2 amino acids 151..162"
XX	XX
WO	WO200037102-A2.
XX	XX
PD	29-JUN-2000.
XX	XX
PF	17-DEC-1999; 99WO-GB004200.
XX	XX
PR	19-DEC-1996; 98GB-00027921.
PR	23-OCT-1999; 99GB-00025015.
XX	XX
PA	(MLM-) ML LAB PLC.
XX	XX
PI	Lechler RI, Rogers NU, Doring A;
XX	XX
DR	WPI; 2000-442537/38.
XX	XX
PT	Novel methods for improving tolerance to a xenograft comprising
PT	immunizing a mammal with a T-cell epitope and a B-cell epitope.
XX	XX
PS	Disclosure, Page 23; 81pp; English.
CC	The present sequence is that of chimeric peptide 6 comprising T-cell
CC	epitope OVA323-339 from chicken egg albumin (ovalbumin) and a B-cell
CC	epitope comprising amino acids 151-162 of pig co-stimulatory molecule

CC CD86 (B7-2) (see AAY95321). The invention relates to a novel strategy for
CC inhibiting costimulation by porcine cells of human T cells, with
CC particular importance in the context of xenotransplantation of porcine
CC organs. Recipients are immunised with hybrid synthetic peptides, such as
CC the present peptide comprising a T cell epitope conjugated to sequences
CC of the porcine costimulatory molecules CD80, CD86 or CD40. Peptides that
CC induce antibodies specific for regions of costimulatory molecules
CC involved in binding to their counter-receptors on human cells are capable
CC of blocking the delivery of costimulation. Once the antibody response has
CC been induced, the transplanted organ will recall this response due to the
CC expression of the costimulatory molecules, thereby sustaining the
CC response, and providing an endogenous mechanism of costimulatory
CC blockade. The method is useful for improving the tolerance of a host to
CC xenografts, particularly porcine pancreatic islet cells. (Updated on 12-
CC SEP-2003 to standardise OS field)
SQ Sequence 29 AA;
Query Match 100.0%; Score 69; DB 3; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.00096;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CSSTQGYPEPQR 12
DB 18 CSSTQGYPEPQR 29
RESULT 2
AAW14944
ID AAW14944 standard; protein; 250 AA.
XX
AC AAW14944;
XX
DT 17-OCT-2003 (revised)
DT 16-JUN-1997 (first entry)
XX
XX Chimeric human/porcine CD86.
DB Chimeric human/porcine CD86.
XX
KM Xenotransplantation; graft rejection; cell interaction; pig; CD86;
KM monoclonal antibody; chimeric antibody; diagnosis.
XX
XX Homo, sapiens.
OS Sus scrofa.
OS Chimeric.
XX
XX Key Location/Qualifiers
XX Peptide 1..25
XX /label= Sig_peptide
XX Protein 26..250
XX /label= Mat_protein
XX Region 246..250
XX /label= Histidine_tag
XX
XX MO9711971-A1.
XX
XX PD 03-APR-1997.
XX
XX PF 27-SEP-1996; 96WO-US015575.
XX
XX PR 28-SEP-1995; 95US-0004489P.
XX PR 26-SEP-1996; 96US-00004489.
XX
XX PA (ALEX-) ALEXION PHARM INC.
XX
XX PI Mueller JP, Evans MJ, Mueller EE, Rollins S, Rother RP, Matis LA;
XX WPI; 1997-212855/19.
XX DR N-PESDB; AAT62939.
XX
XX PT Antibodies binding to porcine but not human cell interaction proteins -
XX useful to treat and assay for rejection of xenografted porcine organs,
XX tissues or cells.

PS Disclosure; Page 69-70; 105pp; English.
XX
XX A chimeric human/porcine CD86 (B7-2) cell adhesion molecule has amino
CC acid residues 1-4 and 197-245 from human CD86, and amino acids 5-196 from
CC porcine CD86. It is encoded by a DNA construct (AAT62939) obt'd. by PCR
CC amplification of porcine sequences and ligation to a sequence encoding
CC the C-terminal region of human CD86 19c domain. A signal sequence
CC facilitates efficient secretion from transfected mammalian cells.
CC Antibodies to porcine CD86 protein, P-selection (see also AAW14945) and
CC vascular cell adhesion molecule (see also AAW14931-42) are useful for
CC diagnosing human rejection of porcine xenotransplants and for improving
CC xenotransplantation of porcine cells, tissues and organs into human
CC recipients. (Updated on 17-OCT-2003 to standardise OS field)
SQ Sequence 250 AA;
Query Match 100.0%; Score 69; DB 2; Length 250;
Best Local Similarity 100.0%; Pred. No. 0.0081;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CSSTQGYPEPQR 12
DB 157 CSSTQGYPEPQR 168
RESULT 3
AAY95321
ID AAY95321 standard; protein; 325 AA.
XX
AC AAY95321;
XX
DT 25-SEP-2000 (first entry)
DT
XX
XX Pig costimulatory molecule CD86 (B7-2).
XX
XX Co-stimulatory molecule; CD86; B7-2; pig; immunosuppressive;
KM xenotransplantation; organ transplant; vaccine; epitope.
XX
XX Sus scrofa.
OS
XX
XX Key Location/Qualifiers
XX Peptide 17..29
XX /note= "peptide 9"
XX Peptide 21..32
XX /note= "peptide 8"
XX Peptide 32..40
XX /note= "peptide 2"
XX Peptide 76..88
XX /note= "peptide 10"
XX Peptide 81..90
XX /note= "peptide 1"
XX Peptide 94..104
XX /note= "peptide 5"
XX Peptide 109..121
XX /note= "peptide 3"
XX Peptide 113..121
XX /note= "peptide 4"
XX Peptide 151..162
XX /note= "peptide 6"
XX
XX WO200037102-A2.
XX
XX PD 29-JUN-2000.
XX
XX PF 17-DEC-1999; 99WO-GB004200.
XX
XX PR 19-DEC-1998; 98GB-00027921.
XX PR 23-OCT-1999; 99GB-0005015.
XX
XX PA (MLML-) ML LAB PLC.
XX
XX PI Lechler RI, Rogers NU, Dorling A;

DR WPI: 2000-442537/38.
DR N-PSDB; AAA95661.
XX Novel methods for improving tolerance to a xenograft comprising
XX immunizing a mammal with a T-cell epitope and a B-cell epitope.
XX
PS Disclosure; Fig 6; 81pp; English.
XX
CC The present sequence is that of pig co-stimulatory molecule CD86 (B7-2),
CC as deduced from an isolated cDNA clone (see AAA95661). CD86 plays a key
CC role in T cell costimulation. The invention relates to a novel strategy
CC for inhibiting costimulation by porcine cells of human T cells, with
CC particular importance in the context of xenotransplantation of porcine
CC organs. Recipients are immunised with hybrid synthetic peptides
CC comprising a T cell epitope conjugated to sequences of the porcine
CC costimulatory molecules CD80, CD86 or CD40, such as peptides 1-10 of CD86
CC (see also AA95325-33). Peptides that induce antibodies specific for
CC regions of costimulatory molecules involved in binding to their counter-
CC receptors on human cells (CD28 and CD14) are capable of blocking the
CC delivery of costimulation. Once the antibody response has been induced,
CC the transplanted organ will recall this response due to the expression of
CC the costimulatory molecules, thereby sustaining the response, and
CC providing an endogenous mechanism of costimulatory blockade. The method
CC is useful for improving the tolerance of costimulatory blockade, particularly
CC particularly porcine pancreatic islet cells
XX
SQ Sequence 325 AA:
XX
Query Match 100.0%; Score 69; DB 3; Length 325;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CSSTQGYPEPQR 12
Db 151 CSSTQGYPEPQR 162
XX
RESULT 4
AA95324
ID AA95324 standard; protein; 325 AA.
XX
AC AA95324;
XX
DT 25-SEP-2000 (first entry)
XX
DE Human costimulatory molecule CD86 (B7-2).
XX
KW Co-stimulatory molecule; CD86; B7-2; human; immunosuppressive;
KW xenotransplantation; organ transplant; vaccine; epitope.
XX
OS Homo sapiens.
XX
XX Location/Qualifiers
FH Key 19..42
FT Peptide /note="epitope"
FT 53..73
FT Peptide /note="epitope"
FT 101..129
FT Peptide /note="epitope"
FT 136..165
FT Peptide /note="epitope"
XX
XX WO200037102-A2.
XX
XX 29-JUN-2000.
XX
XX 17-DEC-1999; 99WO-GB004200.
XX
XX 19-DEC-1998; 98GB-00027921.
XX 23-OCT-1999; 99GB-00025015.
XX
XX (MLML-) ML LAB PLC.
XX

PI Lechler RI, Rogers NJ, Dörfling A;
XX
XX WPI: 2000-442537/38.
DR Novel methods for improving tolerance to a xenograft comprising
XX immunizing a mammal with a T-cell epitope and a B-cell epitope.
XX
PS Disclosure; Fig 26; 81pp; English.
XX
CC The present sequence is that of human co-stimulatory molecule CD86 (B7-
CC 2). CD86 plays a key role in T cell costimulation. The invention relates
CC to a novel strategy for inhibiting costimulation by porcine cells of
CC human T cells, with particular importance in the context of
CC xenotransplantation of porcine organs. Recipients are immunised with
CC hybrid synthetic peptides comprising a T cell epitope conjugated to
CC sequences of the porcine costimulatory molecules CD80, CD86 or CD40 (see
CC AA95321-24). Peptides that induce antibodies specific for regions of
CC costimulatory molecules involved in binding to their counter-receptors on
CC human cells (CD28 and CD14) are capable of blocking the delivery of
CC costimulation. Once the antibody response has been induced, the
CC transplanted organ will recall this response due to the expression of the
CC costimulatory molecules, thereby sustaining the response, and providing
CC an endogenous mechanism of costimulatory blockade. The method is useful
CC for improving the tolerance of a host to xenografts, particularly porcine
CC pancreatic islet cells
XX
SQ Sequence 325 AA:
XX
Query Match 100.0%; Score 69; DB 3; Length 325;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CSSTQGYPEPQR 12
Db 151 CSSTQGYPEPQR 162
XX
RESULT 5
AA941078
ID AA941078 standard; protein; 280 AA.
XX
AC AA941078;
XX
DT 20-DEC-1999 (first entry)
XX
DE Canine B7-2S protein.
XX
KW B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
KW allergic reaction; infectious disease; tumor development; canine;
KW graft rejection; inflammation; arthritis; atopic dermatitis.
XX
XX Canis familiaris.
XX
XX WO9947558-A2.
XX
PD 23-SEP-1999.
XX
PF 19-MAR-1999; 99WO-US006187.
XX
PR 19-MAR-1998; 98US-0078765P.
XX 17-APR-1999; 98US-00062597.
XX
XX (HESK-) HESKA CORP.
XX
XX Sim G, Yang S, Sellins KS;
XX
XX WPI: 1999-571822/48.
XX N-PSDB; AA227921, AA227923.
XX
XX New isolated B7 and CTLA4 nucleic acids, used to develop products for
XX treating, e.g. autoimmune and atopic diseases.
XX
PS Claim 4; Page 109-111; 149pp; English.

XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
 CC encoding nucleic acid molecules from dogs and cats. The proteins can be
 CC expressed by standard recombinant methodology. The nucleic acid molecules
 CC and the encoded proteins can be used for preventing or treating diseases,
 CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
 CC development, graft rejection, inflammation, arthritic and atopic diseases
 CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
 CC cats, cattle, sheep or pets. The products can also be used for detection,
 CC diagnosis and drug screening
 XX
 SQ Sequence 280 AA;
 Query Match 78.3%; Score 54; DB 2; Length 280;
 Best Local Similarity 81.8%; Pred. No. 2.2;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CSSTGYPEPQ 11
 DB 158 CSSTGYPEPK 168
 RESULT 6
 AAY41076
 ID AAY41076 standard; protein, 329 AA.
 XX
 AC AAY41076;
 XX
 DT 20-DEC-1999 (first entry)
 XX
 DE Canine B7-2 protein.
 XX
 KM B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
 KM allergic reaction; infectious disease; tumor development; canine;
 KM graft rejection; inflammation; arthritis; atopic dermatitis.
 XX
 OS Canis familiaris.
 XX
 PN MO9947558-A2.
 XX
 PD 23-SEP-1999.
 XX
 PF 19-MAR-1999; 99WO-US006187.
 XX
 PR 19-MAR-1998; 98US-0078765P.
 PR 17-APR-1998; 98US-00062597.
 XX
 PA (HESK-) HESKA CORP.
 XX
 PI Sim G, Yang S, Sellins KS;
 DR WPI, 1999-571822/48.
 DR N-PSDB; AA27913, AA27915.
 XX
 PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
 PT treating, e.g. autoimmune and atopic diseases.
 XX
 PS Claim 4; Page 97-99; 148pp; English.
 XX
 CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)
 CC encoding nucleic acid molecules from dogs and cats. The proteins can be
 CC expressed by standard recombinant methodology. The nucleic acid molecules
 CC and the encoded proteins can be used for preventing or treating diseases,
 CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
 CC development, graft rejection, inflammation, arthritic and atopic diseases
 CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
 CC cats, cattle, sheep or pets. The products can also be used for detection,
 CC diagnosis and drug screening
 XX
 SQ Sequence 329 AA;
 Query Match 78.3%; Score 54; DB 2; Length 329;
 Best Local Similarity 81.8%; Pred. No. 2.6;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CSSTGYPEPQ 11
 DB 158 CSSTGYPEPK 168
 RESULT 7
 AAY32278
 ID AAY32278 standard; protein, 329 AA.
 XX
 AC AAY32278;
 XX
 DT 12-SEP-2003 (revised)
 DT 15-FEB-2000 (first entry)
 XX
 DE Cat CD86 (B7-2) ligand.
 XX
 KM CD86; B7-2; ligand; cat; vaccine; feline immunodeficiency virus; FIV;
 KM feline leukaemia virus; feline infectious peritonitis virus; FIPV;
 KM feline panleukopenia virus; feline calicivirus; feline reovirus-3;
 KM feline rotavirus; feline coronavirus; feline syncytial virus;
 KM feline sarcoma virus; feline herpesvirus; feline Borna disease;
 KM rabies virus; chlamydia; Toxoplasmosis gondii; Dirofilaria immitis;
 KM parasite; autoimmune disease; transplant rejection; therapy.
 XX
 OS Felis catus.
 XX
 PN WO9957271-A2.
 XX
 PD 11-NOV-1999.
 XX
 PF 30-APR-1999; 99WO-US009502.
 XX
 PR 01-MAY-1996; 98US-00071699.
 XX
 PA (TEXA) TEXAS A & M SYSTEM.
 XX
 PI Collison EW, Hash SM, Choi I;
 DR WPI, 2000-052972/04.
 DR N-PSDB; AA234785.
 XX
 PT Novel feline proteins used to produce feline vaccines which prevent
 PT infectious disease or to promote growth in homologous or heterologous
 PT species.
 XX
 PS Example 1A; Fig 3A; 186pp; English.
 XX
 CC The present sequence represents feline CD86 (B7-2) ligand, as predicted
 CC from isolated cDNA of peripheral blood mononuclear cells. The
 CC coexpression of CD86 with the costimulatory molecules CD28 (see AAY32279)
 CC and a tumour antigen or an antigen from a pathogenic organism has the
 CC ability to activate or enhance activation of T-lymphocytes. Coexpression
 CC of CD86 with CTLA-4 (see AAY32280) has the ability to regulate activation
 CC of T-lymphocytes. The invention provides isolated nucleic acids encoding
 CC feline CD86 ligand, feline CD80 (B7-1) ligand, feline CD28 receptor or
 CC feline CTLA-4 (CD152) receptor, as well as vectors comprising the nucleic
 CC acids, and polypeptides encoded by the nucleic acids. It also provides
 CC vaccines comprising the CD80, CD86, CD28 or CTLA-4 polypeptides and
 CC further comprising immunogens derived from pathogens, especially feline
 CC immunodeficiency virus (FIV), feline leukaemia virus, feline infectious
 CC peritonitis virus, feline panleukopenia virus, feline calicivirus,
 CC feline reovirus-3, feline rotavirus, feline coronavirus, feline syncytial
 CC virus, feline sarcoma virus, feline herpesvirus, feline Borna disease
 CC virus, rabies virus, chlamydia, Toxoplasmosis gondii, Dirofilaria
 CC immitis, or a flea, bacterial pathogen, or parasite (all claimed).
 CC Vaccines capable of enhancing an immune response, and vaccines capable of
 CC suppressing an immune response (suitable for treating an autoimmune
 CC disease or tissue or organ transplant rejection) are claimed. (Updated on
 CC 12-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 329 AA;

Query Match 78.3%; Score 54; DB 3; Length 329;
 Best Local Similarity 81.8%; Pred. No. 2.6;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSSTQGYPEPQ 11
 DB 159 CSSTQGYPEPK 169

RESULT 8

AAV32285 standard; protein; 329 AA.

XX AAV32285;

DT 12-SEP-2003 (revised)

DT 28-FEB-2000 (first entry)

XX Feline CD86 (B7-2).

XX CD86; B7-2; feline; cat; recombinant virus; vaccine; immunomodulator;
 tumor; cancer; therapy.

XX Felis catus.

XX WO957295-A1.

XX 11-NOV-1999.

XX 30-APR-1999; 99WO-US009504.

XX 01-MAY-1998; 98US-00071711.

XX (SCHE) SCHERING-PLOUGH LTD.

XX (SCHE) SCHERING-PLOUGH VETERINARY CORP.

XX Winslow BJ, Cochran MD;

XX WPI: 2000-062155/05.

XX N-PSDB; AAZ34838.

XX Novel recombinant virus useful as immunomodulators, particularly in
 vaccines.

XX Disclosure; Fig 3A; 230pp; English.

XX This sequence represents feline CD86 (B7-2), as deduced from peripheral
 blood mononuclear cell cDNA (see AAZ34838). Manipulating the expression
 of CD28 or CTLA-4 (and/or their co-stimulatory ligands CD80 and CD86)
 regulates T cell proliferation and cytokine release. The invention
 relates to a recombinant virus that contains at least one foreign nucleic
 acid, inserted into a nonessential genomic region, that encodes feline
 CD86, CD80, CD86 or CTLA-4 protein, or their immunogenic fragments, and
 is expressed when the recombinant virus is introduced into a suitable
 host. The invention also provides a recombinant virus further comprising
 a foreign nucleic acid encoding an immunogen derived from a feline
 pathogen; recombinant viruses capable of enhancing an immune response to
 protect against disease; recombinant viruses expressing antitumor
 sequences, capable of suppressing an immune response in a feline, e.g.,
 for treatment of autoimmune disease or transplant rejection; and
 recombinant viruses expressing DNA encoding CD80 and/or CD86 used to
 reduce or eliminate a tumour in cats. (Updated on 12-SEP-2003 to
 standardise OS field)

XX Sequence 329 AA;

Query Match 78.3%; Score 54; DB 3; Length 329;
 Best Local Similarity 81.8%; Pred. No. 2.6;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSSTQGYPEPQ 11
 DB 159 CSSTQGYPEPK 169

DB 159 CSSTQGYPEPK 169

RESULT 9

AAO17734 standard; protein; 329 AA.

XX AAO17734;

DT 08-AUG-2002 (first entry)

XX Feline CD86.

XX Cat; CD28; CD80; CTLA-4; CD86; immunogen; vaccine; viral infection;
 feline immunodeficiency disease; feline infectious peritonitis;
 feline leukaemia virus; cancer; degenerative disease; autoimmune disease;
 virucide; immunomodulator; cytostatic; immunodeficiency.

XX Felis catus.

XX US2002051792-A1.

XX 02-MAY-2002.

XX 30-APR-1999; 99US-00303040.

XX 01-MAY-1998; 98US-0083870P.

XX (MINS/) WINSLOW B J.

XX (COCH/) COCHRAN M D.

XX Winslow BJ, Cochran MD;

XX WPI: 2002-415200/44.

XX N-PSDB; AAL46840.

XX New recombinant virus, useful for immunizing felines to prevent or treat
 feline immunodeficiency virus, comprises foreign nucleic acid encoding
 feline cytotoxic T lymphocyte accessory molecules CD28, CD80, CD86 or
 CTLA-4.

XX Disclosure; Fig 3; 77pp; English.

XX The present invention relates to a recombinant virus comprising at least
 one foreign nucleic acid encoding a protein selected from feline
 cytotoxic T lymphocyte accessory molecules CD28, CD80, CD86 or CTLA-4,
 which is capable of expression when the virus is introduced into an
 appropriate host. The virus can be administered to the feline in order to
 elicit or enhance an immune response to prevent or treat feline
 immunodeficiency disease, feline leukemia, feline infectious peritonitis,
 cancer, degenerative and autoimmune diseases and immunodeficiency. The
 present sequence is a cytotoxic T lymphocyte accessory molecule described
 in the exemplification of the invention

XX Sequence 329 AA;

Query Match 78.3%; Score 54; DB 5; Length 329;
 Best Local Similarity 81.8%; Pred. No. 2.6;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSSTQGYPEPQ 11
 DB 159 CSSTQGYPEPK 169

RESULT 10

AAU78121 standard; protein; 329 AA.

XX AAU78121;

DT 02-JUL-2002 (first entry)


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PD 19-DEC-1996.
XX
XX 06-JUN-1996; 96MO-US009052.
XX
XX 07-JUN-1995; 95US-00479744.
XX
XX (DAND ) DANA FARBER CANCER INST INC.
XX (REFK ) REPLIGEN CORP.
XX
XX Freeman GJ, Nadler LM, Gray GS;
XX
XX WPI; 1997-077269/07.
XX N-PSDB; AAT9198.
XX
XX DNA encoding a B7-2 fusion protein - used to enhance or down regulate B
XX lymphocyte antigens.
XX
XX Example 7D; Page 124; 171pp; English.
XX
XX A cDNA clone (AAT9198) codes for the constant region-like domain
XX (AA08473) of human B-lymphocyte antigen B7-2 (see also AA08467), a
XX CTLA4/CD28 ligand which costimulates T cell activation. It was obtd. by
XX PCR amplification (see also AAT9604-05) and cloned into pNRDSH/IGG1. B7-
XX 2 constant region-IGG1 constant region fusion protein, B7-2CIG, was
XX expressed in COS and CHO cells. Such fusion proteins can be used to
XX suppress T cell-mediated immune responses
XX
XX Sequence 102 AA;
SQ
Query Match 73.9%; Score 51; DB 2; Length 102;
Best Local Similarity 66.7%; Pred. No. 2.4;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 CSSTQGYPEPQR 12
Db 24 CSSTHGYPEPKK 35
RESULT 13
AAB37093
ID AAB37093 standard; protein; 102 AA.
XX
XX AC AAB37093;
XX
XX DT -28-MAR-2001 (first entry)
XX
XX DE Human B7-2 constant domain.
XX
XX KM Immunomodulator; fusion protein; human; murine; mouse; lymphocyte; CD28;
XX antigen; extracellular domain; CTLA4; immunoglobulin constant region;
XX immunogenicity; tumour; sarcoma; antigen presenting cell; macrophage;
XX T cell-mediated immune response; transplantation; vaccination;
XX fusion construct.
XX
XX OS Homo sapiens.
XX
XX PN US6130316-A.
XX
XX PD 10-OCT-2000.
XX
XX PF 26-JUL-1994; 94US-00280757.
XX
XX PR 26-JUL-1993; 93US-00101624.
XX 19-AUG-1993; 93US-00109393.
XX 03-NOV-1993; 93US-00147773.
XX
XX (DAND ) DANA FARBER CANCER INST INC.
XX (REFK ) REPLIGEN CORP.
XX
XX Freeman GJ, Nadler LM, Gray GS, Greenfield B;
XX
XX WPI; 2000-655681/63.
XX N-PSDB; AAC84083.
XX

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XX Nucleic acid and fusion proteins of CTLA4/CD28 ligands, useful for
XX enhancing or suppressing T cell-mediated immune responses, especially
XX during tissue, skin or organ transplantation, or in graft-versus-host
XX disease.
XX
XX Example 7; Col 105-106; 83pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule encoding a
XX fusion protein comprising a first nucleotide sequence encoding a first
XX peptide, and a second nucleotide sequence encoding a second peptide. The
XX first nucleotide sequence hybridizes in 6 X sodium chloride/sodium
XX citrate (SSC) at 45 deg. C, followed by a wash in 0.2 X SSC at 50 deg. C
XX to a portion of a nucleotide sequence which encodes a human or murine B
XX lymphocyte antigen (B7-2) extracellular domain. The first peptide has the
XX ability to bind CD28 or CTLA4. The first peptide has an amino acid
XX sequence that is identical or at least 50% identical with the
XX extracellular domain of a human B7-2 peptide (AA37085). The second
XX peptide is especially an immunoglobulin constant region. This sequence
XX represents the human B7-2 constant domain, used for generating an hb7-
XX 2/19 fusion construct. The nucleic acid molecules are useful in various
XX expression vectors to direct synthesis of the corresponding proteins or
XX peptides in a variety of hosts, particularly eukaryotic cells, e.g.
XX mammalian or insect cell culture. The nucleic acids are also useful for
XX enhancing the immunogenicity of a mammalian cell, e.g. tumour cell
XX (sarcoma) or an antigen presenting cell (macrophage). The fusion proteins
XX or peptides are useful for enhancing or suppressing T cell-mediated
XX immune responses, e.g. in situations of tissue, skin or organ
XX transplantation, or in graft-versus-host disease. The proteins are also
XX useful for enhancing the efficacy of vaccination against a variety of
XX pathogens, and may also be used to upregulate an immune response against
XX a particular pathogen during an infection or against a tumour in a tumour
XX -bearing host
XX
XX Sequence 102 AA;
SQ
Query Match 73.9%; Score 51; DB 3; Length 102;
Best Local Similarity 66.7%; Pred. No. 2.4;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 CSSTQGYPEPQR 12
Db 24 CSSTHGYPEPKK 35
RESULT 14
AAW90209
ID AAW90209 standard; protein; 244 AA.
XX
XX AC AAW90209;
XX
XX DT 10-MAY-1999 (first entry)
XX
XX DE hb7.1his soluble fusion protein.
XX
XX KM B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86;
XX T cell activation; inhibitor; graft versus host disease;
XX transplant rejection; allograft rejection; autoimmune disease; allergy;
XX therapy; human; hb7.1his.
XX
XX OS Homo sapiens.
XX
XX OG Synthetic.
XX
XX CH Chimeric.
XX
XX FH Key
XX FT Peptide
XX FT Domain
XX FT Peptide
XX
XX 1.23 Location/Qualifiers
XX /note= "potential eukaryotic secretory signal peptide"
XX 24..238
XX /note= "human B7.2 (mature protein) extracellular domain"
XX 239..244
XX /note= "histidine detection/purification tag"
XX
XX W09858965-A2.
XX

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XX 30-DEC-1998.
PD 22-JUN-1998; 98WO-EP003791.
XX 20-JUN-1997; 97EP-00870092.
XX (INNO-) INNOGENETICS NV.
XX Lorre K, Sablon E, Buyse M, Bosman A;
XX WPI, 1999-105615/09.
XX New molecules which bind B7.1 and B7.2 - useful to prevent and treat
XX immune diseases including allograft rejection.
XX Example 3.1.3; Fig 5; 182pp; English.
XX This 28 kDa soluble fusion protein, termed hB7.2his, is composed of human
XX co-stimulatory molecule B7.2 extracellular domain fused C-terminally to a
XX hexahistidine detection/purification tag. It was produced by PCR
XX amplification (see AAX01603-04) of hB7.2 cDNA in pCDNA3.2 (TCG2307),
XX insertion of the PCR fragment into baculovirus transfer vector pAcSG2 and
XX expression in Sf9 Spodoptera frugiperda insect cells. The invention
XX relates to molecules such as diabodies, trivalent and tetraivalent
XX antibodies and small antigen binding peptides which can cross-link, or
XX cross-react with, B7.1 and B7.2 expressed on professional antigen
XX presenting cells, leading to the inhibition of antigen-specific T cell
XX activation. Methods to produce such molecules are provided. The molecules
XX are used to treat or prevent diseases of the immune system, in particular
XX graft rejection, graft versus host disease, allergy and autoimmune
XX diseases (claimed)
XX
XX Sequence 244 AA;
SQ
Query Match 73.9%; Score 51; DB 2; Length 244;
Best Local Similarity 66.7%; Pred. No. 5.7;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 CSSTQGYPEPOR 12
Db 151 CSIHGYPEPKK 162
RESULT 15
AAX66005 ID AAX66005 standard; protein; 246 AA.
XX AC AAX66005;
XX 15-MAR-1999 (first entry)
XX Human B7-2 extracellular domain and linker.
XX
XX Tumour interacting protein; cancer; gene therapy; vector; 5T4 antigen;
XX monoclonal antibody; single chain antibody; mouse; human; B7-2;
XX co-stimulatory molecule.
XX Homo sapiens.
XX Synthetic.
XX Chimeric.
XX
XX Key Location/Qualifiers
XX Peptide 1..16
XX Protein /label= Sig_peptide
XX /label= Mat_protein
XX /note= "B7-2 extracellular domain"
XX Peptide 242..246
XX /label= Linker
XX WO9855607-A2.

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PD 10-DEC-1998.
XX 04-JUN-1998; 98WO-GB001627.
XX 04-JUN-1997; 97GB-00011579.
XX 20-JUN-1997; 97GB-00013150.
XX 04-JUL-1997; 97GB-00014230.
XX (OXFO-) OXFORD BIOMEDICA UK LTD.
XX Kingman SM, Bebbington CR, Ellard FM, Carroll MW, Myers KA;
XX WPI, 1999-059910/05.
XX N-PSDB; AAX80293.
XX New vector encoding a tumour interacting protein for treating cancer -
XX contains a desired nucleotide sequence and/or protein which recognises
XX tumours, and is used as a gene delivery system to treat cancer.
XX Example 5; Fig 4; 82pp; English.
XX This polypeptide comprises the extracellular domain (amino acids 1-215)
XX of human co-stimulatory molecule B7-2 joined to a C-terminal flexible
XX peptide linker. It is part of B7-2.5T4.1 co-stimulatory domain, a fusion
XX protein comprising the B7-2 extracellular domain joined via the linker to
XX an scFv (see AAX66002) derived from murine 5T4 monoclonal antibody. B7-
XX 2.5T4.1 cDNA (see AAX80293) can be inserted into vector pCI to allow
XX expression of the fusion protein in mammalian cells. The trophoblast cell
XX surface antigen defined by 5T4 is expressed at high levels on the cells
XX of a wide variety of human tumours. The invention relates to a vector
XX comprising a nucleotide sequence coding for a tumour interacting protein
XX (TIP) and optionally a nucleotide sequence of interest (NOI) which
XX encodes a protein of interest (POI), the vector being capable of
XX delivering the NOI and/or POI to the tumour recognised by the TIP.
XX Delivery can be in vivo or ex vivo. The vector is used to treat cancer,
XX and may also be used as a gene delivery system for introducing at least 1
XX gene encoding a TIP (preferably a tumour binding protein) into a
XX haematopoietic cell lineage. B7-2 is expected to bind specifically to
XX CD28 and CTLA-4 present on human T-cells
XX
XX Sequence 246 AA;
SQ
Query Match 73.9%; Score 51; DB 2; Length 246;
Best Local Similarity 66.7%; Pred. No. 5.7;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 CSSTQGYPEPOR 12
Db 151 CSIHGYPEPKK 162
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Job time : 132.143 secs

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CM protein - protein search, using sw model

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(without alignments)
38.685 Million cell updates/sec

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Perfect score: 69
Sequence: 1 CSSTGYPEPQR 12

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Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/1/aa/5A_COMB.pep:*
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4: /cgn2_6/prodata/1/aa/6B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	69	100.0	325	4	US-09-651-200-20
2	54	78.3	329	4	US-09-651-200-18
3	54	78.3	329	4	US-09-651-200-19
4	54	78.3	329	4	US-09-303-040-6
5	51	73.9	102	3	US-08-479-744A-47
6	51	73.9	102	3	US-08-280-757B-47
7	51	73.9	102	3	US-09-425-762-47
8	51	73.9	323	4	US-09-651-200-21
9	51	73.9	323	4	US-09-441-411-22
10	51	73.9	323	5	PCT-US94-09642-2
11	51	73.9	324	4	US-09-810-174B-6
12	51	73.9	324	4	US-09-620-461-6
13	51	73.9	329	2	US-08-456-104-2
14	51	73.9	329	2	US-08-101-624-2
15	51	73.9	329	3	US-08-479-744A-2
16	51	73.9	329	3	US-08-280-757B-2
17	51	73.9	329	3	US-08-205-697A-23
18	51	73.9	329	3	US-08-102-525-23
19	51	73.9	329	3	US-08-403-253A-4
20	51	73.9	329	4	US-09-667-135-32
21	51	73.9	329	4	US-08-435-816A-4
22	51	73.9	329	4	US-09-425-762-2
23	51	73.9	329	4	US-09-837-867A-23
24	51	73.9	329	4	US-09-206-132-2
25	51	73.9	329	4	US-09-441-411-26
26	51	73.9	329	5	PCT-US95-02576-23
27	51	73.9	351	4	US-09-756-983-18

28	46	66.7	315	4	US-09-910-174B-28	Sequence 28, Appl
29	46	66.7	315	4	US-09-620-461-28	Sequence 28, Appl
30	46	66.7	441	4	US-09-651-200-4	Sequence 4, Appl
31	46	66.7	534	4	US-09-651-200-6	Sequence 6, Appl
32	46	66.7	534	4	US-09-651-200-24	Sequence 24, Appl
33	44	63.8	303	4	US-09-651-200-23	Sequence 23, Appl
34	44	63.8	303	4	US-09-441-411-15	Sequence 15, Appl
35	44	63.8	303	4	US-09-441-411-20	Sequence 20, Appl
36	44	63.8	309	2	US-08-456-104-4	Sequence 4, Appl
37	44	63.8	309	3	US-08-479-744A-23	Sequence 23, Appl
38	44	63.8	309	3	US-08-280-757B-23	Sequence 23, Appl
39	44	63.8	309	3	US-08-205-697A-21	Sequence 21, Appl
40	44	63.8	309	3	US-08-702-525-21	Sequence 21, Appl
41	44	63.8	309	4	US-09-651-200-22	Sequence 22, Appl
42	44	63.8	309	4	US-09-667-135-33	Sequence 33, Appl
43	44	63.8	309	4	US-09-425-762-23	Sequence 23, Appl
44	44	63.8	309	4	US-09-837-867A-21	Sequence 21, Appl
45	44	63.8	309	4	US-09-206-132-4	Sequence 4, Appl

ALIGNMENTS

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RESULT 1
US-09-651-200-20
; Sequence 20, Application US/09651200
; Patent No. 6429303
; GENERAL INFORMATION:
; APPLICANT: Green et al
; TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B
; TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and
; FILE REFERENCE: 15966-562 (CURA-62)
; CURRENT APPLICATION NUMBER: US/09/651,200
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/152383
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/172909
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/183578
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 325
; TYPE: PRT
; ORGANISM: sus sp.
US-09-651-200-20

Query Match          100.0%; Score 69; DB 4; Length 325;
Best local similarity 100.0%; Pred. No. 0.0013;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1  CSSTGYPEPQR 12
Db      151 CSSTGYPEPQR 162

RESULT 2
US-09-651-200-18
; Sequence 18, Application US/09651200
; Patent No. 6429303
; GENERAL INFORMATION:
; APPLICANT: Green et al
; TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B
; TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and
; FILE REFERENCE: 15966-562 (CURA-62)
; CURRENT APPLICATION NUMBER: US/09/651,200
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/152383
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/172909

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; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/183578
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Felis catus
; US-09-651-200-18

Query Match
Best Local Similarity 78.3%; Score 54; DB 4; Length 329;
Best Local Similarity 81.8%; Pred. No. 0.36;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSSTQGYPEPQ 11
Db 159 CSSTQGYPEPK 169

RESULT 3
US-09-651-200-19
; Sequence 19, Application US/09651200
; Patent No. 6429303
; GENERAL INFORMATION:
; APPLICANT: Green et al
; TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B
; TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 15966-562 (CURA-62)
; CURRENT APPLICATION NUMBER: US/09/651,200
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/152383
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/172909
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/183578
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Canis familiaris
; US-09-651-200-19

Query Match
Best Local Similarity 78.3%; Score 54; DB 4; Length 329;
Best Local Similarity 81.8%; Pred. No. 0.36;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSSTQGYPEPQ 11
Db 158 CSSTQGYPEPK 168

RESULT 4
US-09-303-040-6
; Sequence 6, Application US/09303040
; Patent No. 6555671
; GENERAL INFORMATION:
; APPLICANT: Winslow, Barbara J.
; TITLE OF INVENTION: Recombinant Virus Expressing Foreign DNA Encoding
; TITLE OF INVENTION: Feline CD80, Feline CD86, Feline CTLA-4 or
; TITLE OF INVENTION: Feline Interferon-gamma And Uses Thereof
; FILE REFERENCE: 54957-B
; CURRENT APPLICATION NUMBER: US/09/303,040
; PRIOR FILING DATE: 1999-04-30
; EARLIER APPLICATION NUMBER: 60/083,870
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
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; LENGTH: 329
; TYPE: PRT
; ORGANISM: feline CD86
; US-09-303-040-6

Query Match
Best Local Similarity 78.3%; Score 54; DB 4; Length 329;
Best Local Similarity 81.8%; Pred. No. 0.36;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSSTQGYPEPQ 11
Db 159 CSSTQGYPEPK 169

RESULT 5
US-08-479-744A-47
; Sequence 47, Application US/08479744A
; Patent No. 6084067
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: No. 6084067e1 CTLA4/CD28 Ligands and
; TITLE OF INVENTION: Uses Therefor
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,744A
; FILING DATE: June 7, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/280,757
; FILING DATE: 26-JUL-1994
; APPLICATION NUMBER: 08/109,393
; FILING DATE: 28-AUG-1993
; APPLICATION NUMBER: 08/101,624
; FILING DATE: 26-JULY-1993
; APPLICATION NUMBER: 08/147,773
; FILING DATE: 3-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-004CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 102 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-479-744A-47

Query Match
Best Local Similarity 73.9%; Score 51; DB 3; Length 102;
Best Local Similarity 66.7%; Pred. No. 0.34;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTQGYPEPQ 12
Db 24 CSSTQGYPEPK 35
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Thu Dec 16 12:21:12 2004

us-09-868-605-14_copy_151_162.rat

Page 3

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RESULT 6
US-08-280-757B-47
; Sequence 47, Application US/08280757B
; Patent No. 6130316
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; APPLICANT: Gray, Gary S.
; APPLICANT: Greenfield, Edward
; TITLE OF INVENTION: No. 6130316 CTLA4/CD28 Ligands and
; TITLE OF INVENTION: Uses Therefor
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/280,757B
; FILING DATE: 26-JUL-1994
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/101,624
; FILING DATE: 26-JUL-1993
; APPLICATION NUMBER: 08/109,393
; FILING DATE: 19-AUG-1993
; APPLICATION NUMBER: 08/147,773
; FILING DATE: 3-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-004CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 102 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-280-757B-47

Query Match 73.9%; Score 51; DB 3; Length 102;
Best Local Similarity 66.7%; Pred. No. 0.34;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTGYEPPOR 12
DB 24 CSSTHGYEPPK 35
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STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/425,762
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/479,744
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-004CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 102 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-425-762-47

Query Match 73.9%; Score 51; DB 4; Length 102;
Best Local Similarity 66.7%; Pred. No. 0.34;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTGYEPPOR 12
DB 24 CSSTHGYEPPK 35

RESULT 8
US-09-651-200-21
; Sequence 21, Application US/09651200
; Patent No. 6429303
; GENERAL INFORMATION:
; APPLICANT: Green et al
; TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B
; TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and
; FILE REFERENCE: 15966-562 (CURA-62)
; CURRENT APPLICATION NUMBER: US/09/651,200
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/152383
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/172909
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/183578
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 21
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-651-200-21

Query Match 73.9%; Score 51; DB 4; Length 323;
Best Local Similarity 66.7%; Pred. No. 1.1;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTGYEPPOR 12
DB 24 CSSTHGYEPPK 35
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Db 151 CSISNGYPEPKK 162

RESULT 9

US-09-441-411-22
Sequence 22, Application US/09441411
Patent No. 6734172
GENERAL INFORMATION:
APPLICANT: Scholler, Nathalie B.
APPLICANT: Disis, Mary L.
APPLICANT: Helstrom, Ingegerd
APPLICANT: Helstrom, Karl Erik
TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
FILE REFERENCE: 730033.409
CURRENT APPLICATION NUMBER: US/09/441.411
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22
LENGTH: 323
TYPE: PRT
ORGANISM: Homo sapiens
US-09-441-411-22

Query Match

Best Local Similarity 73.9%; Score 51; DB 4; Length 323;
Best Local Similarity 66.7%; Pred. No. 1.1;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTGYPEPKR 12

Db 151 CSISNGYPEPKK 162

RESULT 10

PCT-US94-09642-2
Sequence 2, Application PC/TUS9409642
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Purified Mammalian CTLA-4 Binding
TITLE OF INVENTION: Protein and Related Reagents
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: Schering-Plough Corporation, M-3-W
STREET: One Giralda Farms
CITY: Madison
STATE: New Jersey
COUNTRY: USA
ZIP: 07940-1000
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh IIcx
OPERATING SYSTEM: System Software 7.1
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09642
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/120,606
FILING DATE: 13-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/116,882
FILING DATE: 03-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Blaisdale, John H. C.
REGISTRATION NUMBER: 31,895
REFERENCE/DOCKET NUMBER: DX0390X1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-822-7398
TELEFAX: 201-822-7039
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 323 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-09642-2

Query Match

Best Local Similarity 73.9%; Score 51; DB 5; Length 323;
Best Local Similarity 66.7%; Pred. No. 1.1;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTGYPEPKR 12

Db 151 CSISNGYPEPKK 162

RESULT 11

US-09-910-174B-6
Sequence 6, Application US/09910174B
Patent No. 6630575
GENERAL INFORMATION:
APPLICANT: Coyle, Anthony J.
APPLICANT: Frazer, Christopher C.
APPLICANT: Manning, Stephen
TITLE OF INVENTION: B7-H2 Molecules, No. 6630575el Members of the B7
TITLE OF INVENTION: Family and Uses Thereof
FILE REFERENCE: 35800/236924
CURRENT APPLICATION NUMBER: US/09/910,174B
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: 2001-07-20
PRIOR FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 324
TYPE: PRT
ORGANISM: Homo sapiens
US-09-910-174B-6

Query Match

Best Local Similarity 73.9%; Score 51; DB 4; Length 324;
Best Local Similarity 66.7%; Pred. No. 1.1;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTGYPEPKR 12

Db 151 CSISNGYPEPKK 162

RESULT 12

US-09-620-461-6
Sequence 6, Application US/09620461
Patent No. 6635750
GENERAL INFORMATION:
APPLICANT: Coyle, Anthony J.
APPLICANT: Frazer, Christopher C.
APPLICANT: Manning, Stephen
TITLE OF INVENTION: B7-H2 Molecules, No. 6635750el Members of the B7
TITLE OF INVENTION: Family and Uses Thereof
FILE REFERENCE: 5800-149
CURRENT APPLICATION NUMBER: US/09/620,461
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 324
TYPE: PRT
ORGANISM: Homo sapiens
US-09-620-461-6

Query Match

Best Local Similarity 73.9%; Score 51; DB 4; Length 324;
Best Local Similarity 66.7%; Pred. No. 1.1;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTGYPEPKR 12

Db 151 CSISNGYPEPKK 162

Db 151 CSSTGYPEPK 162

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RESULT 13
US-08-456-104-2
; Sequence 2, Application US/08456104
; Patent No. 5861310
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASED
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,104
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/101,624;
; FILING DATE: 26-JUL-1993;
; APPLICATION NUMBER: 08/109,393;
; APPLICATION NUMBER: 19-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 329 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-456-104-2
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Query Match 73.9%; Score 51; DB 2; Length 329;
Best Local Similarity 66.7%; Pred. No. 1.1;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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QY 1 CSSTGYPEPK 12
Db 157 CSSTGYPEPK 168
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RESULT 14
US-08-101-624-2
; Sequence 2, Application US/08101624
; Patent No. 5942607
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: No. 5942607el CTLA4/CD28 ligands and
; TITLE OF INVENTION: Uses Therefor
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
```

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STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/101,624
; FILING DATE: 26-JUL-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 329 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-101-624-2
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Query Match 73.9%; Score 51; DB 2; Length 329;
Best Local Similarity 66.7%; Pred. No. 1.1;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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QY 1 CSSTGYPEPK 12
Db 157 CSSTGYPEPK 168
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RESULT 15
US-08-479-744A-2
; Sequence 2, Application US/08479744A
; Patent No. 6084067
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: No. 6084067el CTLA4/CD28 ligands and
; TITLE OF INVENTION: Uses Therefor
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,744A
; FILING DATE: June 7, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/280,757
; FILING DATE: 26-JUL-1994
; APPLICATION NUMBER: 08/109,393
; FILING DATE: 28-AUG-1993
; APPLICATION NUMBER: 08/101,624
; FILING DATE: 26-JULY-1993
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APPLICATION NUMBER: 08/147,773
FILING DATE: 3-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mandagouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-004CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 329 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-479-744A-2

Query Match 73.9%; Score 51; DB 3; Length 329;
Best Local Similarity 66.7%; Pred. No. 1.1;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

CY 1 CSSTQGYPEPOR 12
||| |||||:
Db 157 CSSTHGYPEPKK 168

Search completed: December 15, 2004, 16:38:41
Job time : 20.5714 secs

Thu Dec 16 12:21:12 2004

us-09-868-605-14_copy_151_162.rapb

Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 15, 2004, 16:37:44 ; Search time 116.571 Seconds
(without alignments)
36.768 Million cell updates/sec

Title: US-09-868-605-14_COPY_151_162
Perfect score: 69
Sequence: 1 CSSTGQYEPFQR 12

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Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database :

Published Applications AA: *
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10: /cgn2_6/prodata/2/pubpaa/US09C_PUBCOMB.pep: *
11: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pep: *
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	54	78.3	280	16	US-10-790-396-17
2	54	78.3	329	9	US-09-303-510-6
3	54	78.3	329	9	US-09-303-040-6
4	54	78.3	329	16	US-10-790-396-7
5	54	78.3	332	16	US-10-790-396-26
6	51	73.9	102	9	US-09-425-762-47
7	51	73.9	219	9	US-09-915-789A-22
8	51	73.9	246	16	US-10-334-235-40
9	51	73.9	260	9	US-08-845-899A-5
10	51	73.9	323	9	US-09-955-866-5
11	51	73.9	323	9	US-09-896-738-11
12	51	73.9	323	9	US-09-915-789A-16
13	51	73.9	323	10	US-09-441-411-22

14	51	73.9	323	13	US-10-087-192-1080	Sequence 1080, App
15	51	73.9	323	14	US-10-207-655-121	Sequence 121, App
16	51	73.9	323	17	US-10-762-128-22	Sequence 22, App
17	51	73.9	323	17	US-10-276-642-16	Sequence 16, App
18	51	73.9	324	9	US-09-910-174A-6	Sequence 6, App
19	51	73.9	324	16	US-10-644-671-6	Sequence 6, App
20	51	73.9	329	8	US-08-592-711-4	Sequence 4, App
21	51	73.9	329	9	US-09-183-055-4	Sequence 2, App
22	51	73.9	328	9	US-09-425-762-2	Sequence 2, App
23	51	73.9	328	9	US-09-837-867A-23	Sequence 23, App
24	51	73.9	329	10	US-09-441-411-26	Sequence 26, App
25	51	73.9	329	10	US-09-962-968-23	Sequence 23, App
26	51	73.9	329	10	US-09-350-202-4	Sequence 4, App
27	51	73.9	329	14	US-10-041-319-8	Sequence 8, App
28	51	73.9	329	15	US-10-390-330-4	Sequence 4, App
29	51	73.9	329	15	US-10-318-885-32	Sequence 32, App
30	51	73.9	329	17	US-10-643-768-23	Sequence 23, App
31	51	73.9	329	17	US-10-756-783-6	Sequence 6, App
32	51	73.9	329	17	US-10-762-128-26	Sequence 26, App
33	51	73.9	329	17	US-10-429-079B-2	Sequence 2, App
34	51	73.9	351	9	US-09-756-983-18	Sequence 18, App
35	51	73.9	351	17	US-10-614-639A-18	Sequence 18, App
36	47	68.1	453	16	US-10-403-142-136	Sequence 136, App
37	46	66.7	216	9	US-09-789-561-158	Sequence 158, App
38	46	66.7	216	9	US-09-790-622-8	Sequence 8, App
39	46	66.7	216	14	US-10-141-953-8	Sequence 8, App
40	46	66.7	216	16	US-10-403-142-152	Sequence 152, App
41	46	66.7	244	9	US-09-790-622-7	Sequence 7, App
42	46	66.7	244	14	US-10-141-953-7	Sequence 7, App
43	46	66.7	315	9	US-09-910-174A-28	Sequence 28, App
44	46	66.7	315	16	US-10-644-671-28	Sequence 28, App
45	46	66.7	315	17	US-10-484-122-6	Sequence 6, App

ALIGNMENTS

RESULT 1
US-10-790-396-17
Sequence 17, Application US/10790396
Publication No. US20040157296A1
GENERAL INFORMATION:
APPLICANT: Yang, Gek-see
APPLICANT: Yung, Shunlin
APPLICANT: Sellins, Karen S.
TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY
PROTEINS, NUCLEIC
FILE REFERENCE: IM-1-C1-PCT
CURRENT APPLICATION NUMBER: US/10790,396
CURRENT FILING DATE: 2004-03-01
PRIOR APPLICATION NUMBER: US/09/646,561
PRIOR FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: 60/078,765
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 09/062,597
PRIOR FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 280
TYPE: PRT
ORGANISM: Canis familiaris
US-10-790-396-17
Query Match
Best Local Similarity 78.3%; Score 54; DB 16; Length 280;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
1 CSSTGQYEPFQR 11
158 CSSTGQYEPFQR 168

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RESULT 2
US-09-303-510-6
; Sequence 6, Application US/09303510A
; Patent No. US20020028208A1
; GENERAL INFORMATION:
; APPLICANT: Collisson, Ellen W.
; APPLICANT: Hash, Stephen M.
; APPLICANT: Choi, Insoo
; TITLE OF INVENTION: Feline CD80, Feline CD86, Feline CD28, and Feline
; FILE REFERENCE: CTLA-4 Nucleic Acid and Polypeptides
; FILE REFERENCE: 54354
; CURRENT APPLICATION NUMBER: US/09/303,510A
; EARLIER FILING DATE: 1999-04-30
; EARLIER APPLICATION NUMBER: 60/083,869
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Feline
US-09-303-510-6

Query Match
Best Local Similarity 78.3%; Score 54; DB 9; Length 329;
Best Local Similarity 81.8%; Pred. No. 1.3;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSSTOQYPEPQ 11
DB 159 CSSTOQYPEPK 169

RESULT 3
US-09-303-040-6
; Sequence 6, Application US/09303040
; Patent No. US20020051792A1
; GENERAL INFORMATION:
; APPLICANT: Winslow, Barbara J.
; APPLICANT: Cochran, Mark D.
; TITLE OF INVENTION: Recombinant Virus Expressing Foreign DNA Encoding
; TITLE OF INVENTION: Feline CD80, Feline CD86, Feline CD28, Feline CTLA-4 or
; FILE REFERENCE: 54957-B
; CURRENT APPLICATION NUMBER: US/09/303,040
; CURRENT FILING DATE: 1999-04-30
; EARLIER APPLICATION NUMBER: 60/083,870
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Feline CD86
US-09-303-040-6

Query Match
Best Local Similarity 78.3%; Score 54; DB 9; Length 329;
Best Local Similarity 81.8%; Pred. No. 1.3;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSSTOQYPEPQ 11
DB 159 CSSTOQYPEPK 169

RESULT 4
US-10-790-396-7
; Sequence 7, Application US/10790396
; Publication No. US20040157296A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Sellins, Karen S.
; TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY
; TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY PROTEINS, NUCLEIC
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; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-1-C1-PCT
; CURRENT APPLICATION NUMBER: US/10/790,396
; CURRENT FILING DATE: 2004-03-01
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/078,765
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 09/062,597
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-790-396-7

Query Match
Best Local Similarity 78.3%; Score 54; DB 16; Length 329;
Best Local Similarity 81.8%; Pred. No. 1.3;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSSTOQYPEPQ 11
DB 158 CSSTOQYPEPK 168

RESULT 5
US-10-790-396-26
; Sequence 26, Application US/10790396
; Publication No. US20040157296A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Sellins, Karen S.
; TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-1-C1-PCT
; CURRENT APPLICATION NUMBER: US/10/790,396
; CURRENT FILING DATE: 2004-03-01
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/078,765
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 09/062,597
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Felis catus
US-10-790-396-26

Query Match
Best Local Similarity 78.3%; Score 54; DB 16; Length 332;
Best Local Similarity 81.8%; Pred. No. 1.4;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSSTOQYPEPQ 11
DB 159 CSSTOQYPEPK 169

RESULT 6
US-09-425-762-47
; Sequence 47, Application US/09425762
; Publication No. US20020086414A1
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: No. 6605279e1 CTLA4/CD28 Ligands and
; TITLE OF INVENTION: Uses Therefor
```


NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/425,762
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,744
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-004CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-425-762-47

Query Match 73.9% Score 51; DB 9; Length 102;
Best Local Similarity 66.7%; Pred. No. 1.3;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTGYPEPOR 12
DB 24 CSIHGYPEPKX 35

RESULT 7
US-09-915-789A-22
Sequence 22, Application US/09915789A
Patent No. US20020168762A1
GENERAL INFORMATION:
APPLICANT: Chen, Lieping
TITLE OF INVENTION: B7-H3 AND B7-H4, NOVEL IMMUNOREGULATORY
FILE OF INVENTION: MOLECULES
FILE REFERENCE: 07035-219001
CURRENT APPLICATION NUMBER: US/09/915,789A
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 60/220,991
PRIOR FILING DATE: 2000-07-27
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22
LENGTH: 219
TYPE: PRT
ORGANISM: Homo sapiens
US-09-915-789A-22

Query Match 73.9% Score 51; DB 9; Length 219;
Best Local Similarity 66.7%; Pred. No. 2.8;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTGYPEPOR 12
DB 129 CSIHGYPEPKX 140

RESULT 8
US-10-334-235-40
Sequence 40, Application US/10334235
Publication No. US20040131591A1
GENERAL INFORMATION:
APPLICANT: Oxford Biomedica (UK) Ltd.
APPLICANT: Kingsman, Alan
APPLICANT: Bebbington, Christopher
APPLICANT: Carroll, Miles
APPLICANT: Ellard, Fiona
APPLICANT: Kingsman, Susan
APPLICANT: Myers, Kevin
APPLICANT: Lamikandra, Abigail
TITLE OF INVENTION: VECTOR SYSTEM
FILE REFERENCE: 53268200920
CURRENT APPLICATION NUMBER: US/10/334,235
CURRENT FILING DATE: 2002-12-30
PRIOR APPLICATION NUMBER: US 10/060,585
PRIOR FILING DATE: 2002-01-29
PRIOR APPLICATION NUMBER: PCT/GB00/04317
PRIOR FILING DATE: 2000-11-13
PRIOR APPLICATION NUMBER: US 09/445,375
PRIOR FILING DATE: 1998-06-04
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 40
LENGTH: 246
TYPE: PRT
ORGANISM: Homo sapiens
US-10-334-235-40

Query Match 73.9% Score 51; DB 16; Length 246;
Best Local Similarity 66.7%; Pred. No. 3.1;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTGYPEPOR 12
DB 151 CSIHGYPEPKX 162

RESULT 9
US-09-845-899A-5
Sequence 5, Application US/09845899A
Patent No. US20020147326A1
GENERAL INFORMATION:
APPLICANT: CHAIKIN, MARGERY ANN
APPLICANT: LYNN, SALLY DOREEN PATRICIA
APPLICANT: SWEET, RAYMOND W.
APPLICANT: TRUEN, ALEMESEGED
TITLE OF INVENTION: HEXAMERIC FUSION PROTEINS AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: P50496
CURRENT APPLICATION NUMBER: US/09/845,899A
CURRENT FILING DATE: 2001-04-30
PRIOR APPLICATION NUMBER: 09/202,346
PRIOR FILING DATE: 1999-01-13
PRIOR APPLICATION NUMBER: US 60/043,948
PRIOR FILING DATE: 1997-02-19
PRIOR APPLICATION NUMBER: US 60/038,915
PRIOR FILING DATE: 1997-02-21
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 5
LENGTH: 260
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-845-899A-5

Query Match 73.9% Score 51; DB 9; Length 260;
Best Local Similarity 66.7%; Pred. No. 3.3;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTGYPEPOR 12
DB 129 CSIHGYPEPKX 140

Qy 1 CSSTOGEPPOR 12
Db 157 CSIHGPEPKK 168

RESULT 10

US-09-955-866-5
; Sequence 5, Application US/09955866
; Patent No. US20020107363A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Michael
; APPLICANT: Sullivan, John K.
; APPLICANT: Holst, Paige
; APPLICANT: Yoshinaga, Steven Kiyoshi
; TITLE OF INVENTION: B7-Like Polypeptides and Uses Thereof
; FILE REFERENCE: 00,759-A
; CURRENT APPLICATION NUMBER: US/09/955,866
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/233,867
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-955-866-5

Query Match 73.9%; Score 51; DB 9; Length 323;
Best Local Similarity 66.7%; Pred. No. 4.1;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CSSTOGEPPOR 12
Db 151 CSIHGPEPKK 162

RESULT 11

US-09-896-738-11
; Sequence 11, Application US/09896738
; Patent No. US20020165347A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Michael
; APPLICANT: Sullivan, John K.
; APPLICANT: Fang, Mei
; TITLE OF INVENTION: B7-Like Molecules and Uses Thereof
; FILE REFERENCE: 00-513-A
; CURRENT APPLICATION NUMBER: US/09/896,738
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/215,645
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-896-738-11

Query Match 73.9%; Score 51; DB 9; Length 323;
Best Local Similarity 66.7%; Pred. No. 4.1;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CSSTOGEPPOR 12
Db 151 CSIHGPEPKK 162

RESULT 12
US-09-915-789A-16
; Sequence 16, Application US/09915789A
; Patent No. US20020168762A1
; GENERAL INFORMATION:

; APPLICANT: Chen, Lieping
; TITLE OF INVENTION: B7-H3 AND B7-H4, NOVEL IMMUNOREGULATORY
; TITLE OF INVENTION: MOLECULES
; FILE REFERENCE: 07039-219001
; CURRENT APPLICATION NUMBER: US/09/915,789A
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/220,991
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-789A-16

Query Match 73.9%; Score 51; DB 9; Length 323;
Best Local Similarity 66.7%; Pred. No. 4.1;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CSSTOGEPPOR 12
Db 151 CSIHGPEPKK 162

RESULT 13

US-09-441-411-22
; Sequence 22, Application US/09441411
; Publication No. US20030008342A1
; GENERAL INFORMATION:
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Disis, Mary L.
; APPLICANT: Hellstrom, Ingegerd
; APPLICANT: Hellstrom, Karl Erik
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 730033,409
; CURRENT APPLICATION NUMBER: US/09/441,411
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-441-411-22

Query Match 73.9%; Score 51; DB 10; Length 323;
Best Local Similarity 66.7%; Pred. No. 4.1;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CSSTOGEPPOR 12
Db 151 CSIHGPEPKK 162

RESULT 14

US-10-087-192-1080
; Sequence 1080, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 52945200012
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1080
LENGTH: 323
TYPE: PRT
ORGANISM: Homo sapiens
US-10-087-192-1080

Query Match 73.9%; Score 51; DB 13; Length 323;
Best Local Similarity 66.7%; Pred. No. 4.1;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTGYPPRQ 12
DB 151 CSIHGYPPPK 162

RESULT 15
US-10-207-655-121
Sequence 121, Application US/10207655
Publication No. US20030118592A1
GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069, 401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patent version 3.0
SEQ ID NO 121
LENGTH: 323
TYPE: PRT
ORGANISM: Homo sapiens
US-10-207-655-121

Query Match 73.9%; Score 51; DB 14; Length 323;
Best Local Similarity 66.7%; Pred. No. 4.1;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTGYPPRQ 12
DB 151 CSIHGYPPPK 162

Search completed: December 15, 2004, 16:54:14
Job time: 117.571 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 15, 2004, 16:28:26 ; Search time 14.2857 Seconds
(without alignments)
80.822 Million cell updates/sec

Title: US-09-868-605-14_COPY_151_162
Perfect score: 69
Sequence: 1 CSSTGQGYPEPQR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR 79: *
2: PIR: *
3: PIR: *
4: PIR: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	82.6	330	2	CD86 precursor - r
2	51	73.9	275	2	CD86 spliced varia
3	51	73.9	328	1	B7-2 antigen - hum
4	44	63.8	309	2	gene B7-2 protein
5	44	63.8	579	2	hypothetical prote
6	42	60.9	92	2	hypothetical prote
7	42	60.9	239	2	CD80 precursor - r
8	42	60.9	487	2	butyrophilin - mou
9	41	59.4	268	2	B-cell-restricted
10	41	59.4	288	2	B7 protein - red-c
11	41	59.4	526	2	butyrophilin precu
12	41	59.4	526	2	butyrophilin - bov
13	40	58.0	423	2	hypothetical prote
14	40	58.0	1273	2	sax-3 protein - Ca
15	39	56.5	215	2	hibernation-relate
16	39	56.5	323	2	conserved hypotet
17	39	56.5	470	2	hypothetical prote
18	39	56.5	827	2	SOX6 protein - mou
19	38	55.1	100	2	hypothetical prote
20	38	55.1	142	2	hypothetical 16X p
21	38	55.1	142	2	hypothetical prote
22	38	55.1	142	2	hypothetical prote
23	38	55.1	164	2	hypothetical prote
24	38	55.1	307	2	homeotic protein H
25	38	55.1	374	2	probable RNA bindi
26	38	55.1	378	2	hypothetical prote
27	38	55.1	378	2	hypothetical prote
28	38	55.1	841	2	hypothetical prote
29	38	55.1	1040	2	receptor tyrosine

30	38	55.1	1103	2	T22889	hypothetical prote
31	38	55.1	1747	2	A54121	collagen alpha-4 c
32	38	55.1	1906	1	S68235	myosin-light-chain
33	38	55.1	2715	2	T13049	eyelid - fruit fly
34	37	53.6	92	2	T15501	hypothetical prote
35	37	53.6	207	1	PUPG	neuroendocrine pro
36	37	53.6	210	2	A49745	neuroendocrine pro
37	37	53.6	212	1	PURU	neuroendocrine pro
38	37	53.6	212	2	S12477	neuroendocrine pro
39	37	53.6	219	2	A82498	Cdbv family protei
40	37	53.6	237	2	T36722	probable membrane
41	37	53.6	259	2	AE3411	hypothetical prote
42	37	53.6	301	2	G83182	hypothetical prote
43	37	53.6	379	2	A35669	Gene CyR61 protein
44	37	53.6	391	2	T09058	butyrophilin homol
45	37	53.6	431	2	T38471	probable chromatin

ALIGNMENTS

RESULT 1
146691
CD86 precursor - rabbit
C.Species: Oryctolagus cuniculus (domestic rabbit)
C.Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004
C.Accession: 146691
R.Isono, T.; Seto, A.
Immunogenetics 42, 217-220, 1995
A.Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecu
A.Reference number: 146689; MUID:95369849; PMID:7642234
A.Accession: 146691
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: mRNA
A.Residues: 1-330 <ISO>
A.Reference: UNIPROT:P42071; GB:D49842; NID:9755098; PIDN:BA00642.1; PID:975509
C.Superfamily: B7-2 antigen

Query Match 82.6%; Score 57; DB 2; Length 330;
Best Local Similarity 75.0%; Pred. No. 0.036;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSSTGQGYPEPQR 12
DB 157 CSSVQGYPEPKK 168

RESULT 2

UC7604
CD86 spliced variant CD86 deltaTM isoform - human
C.Species: Homo sapiens (man)
C.Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 18-Nov-2002
C.Accession: UC7604
R.Magistrelli, G.; Caron, G.; Gauchat, J.F.; Jeanmin, P.; Bonnefoy, J.Y.; Delneste, Y.
Biochem. Biophys. Res. Commun. 280, 1211-1215, 2001
A.Title: Identification of an alternatively spliced variant of human CD86 mRNA.
A.Reference number: UC7604; MUID:21092744; PMID:11162656
A.Accession: UC7604
A.Molecule type: mRNA
A.Residues: 1-275 <MAG>
A.Comment: This CD86 variant expressed by activated human monocytes, is a costimulatory
C.Genetics:
A.Gene: cd86deltaTM
C.Superfamily: B-Lymphocyte restricted antigen B7
C.Keywords: immune response

Query Match 73.9%; Score 51; DB 2; Length 275;
Best Local Similarity 66.7%; Pred. No. 0.32;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTGQGYPEPQR 12
DB 151 CSSTGQGYPEPKK 162

RESULT 3

B7-2 antigen - human
A:Accession: A48754
M:Alternate names: B70 glycoprotein; CD86 antigen; CTLA-4 counter-receptor
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A48754; #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
R:Freeman, G.J.; Gribben, J.G.; Boussiotis, V.A.; Ng, J.W.; Restivo Jr., V.A.; Lombard, S.; Science 262, 909-911, 1993
A:Title: Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human T cell proliferation
A:Reference number: A48754; PMID:94053735; PMID:7694363
A:Accession: A48754
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-329 <FR>
A:Cross-references: UNIPROT:P42081; GB:L25259; NID:g416368; PIDN:AAA58389.1; PID:g416368
A:Note: It is uncertain whether Met-1 or Met-7 is the initiator
R:Azuma, M.; Ito, D.; Yagita, H.; Okumura, K.; Phillips, J.H.; Ianier, L.L.; Somoza, C.; Nature 366, 76-79, 1993
A:Title: B70 antigen is a second ligand for CTLA-4 and CD28.
A:Reference number: S39055; PMID:94050123; PMID:7694153
A:Accession: S39055
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 7-329 <AZ>
A:Cross-references: GB:U04343; NID:g439838; PIDN:AAH0314.1; PID:g439839
C:Genetics:
A:Gene: GDB:CD86; CD28LG2
A:Cross-references: GDB:433597; OMIM:601020
A:Map position: 3q13.3-q21
C:Superfamily: B7-2 antigen
C:Keywords: glycoprotein

Query Match 73.9%; Score 51; DB 1; Length 329;
Best Local Similarity 66.7%; Pred. No. 0.38;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTGYPEP 12
DB 157 CSSTGYPEP 168

RESULT 4

gene B7-2 protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: 149522
R:Freeman, G.J.; Bortello, F.; Hodes, R.J.; Reiser, H.; Gribben, J.G.; Ng, J.W.; Kim, J.; Exp. Med. 178, 2185-2192, 1993
A:Title: Murine B7-2, an alternative CTLA4 counter-receptor that costimulates T cell proliferation
A:Reference number: 149522; PMID:9405585; PMID:7504053
A:Accession: 149522
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-309 <RB>
A:Cross-references: UNIPROT:P42082; GB:L25506; NID:g432478; PIDN:AAA79770.1; PID:g432478
C:Genetics:
A:Gene: B7-2
C:Superfamily: B7-2 antigen

Query Match 63.8%; Score 44; DB 2; Length 309;
Best Local Similarity 50.0%; Pred. No. 5.7;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSSTGYPEP 12
DB 157 CSSTGYPEP 168

RESULT 5

T30635
hypothetical protein 33L - Molluscum contagiosum virus 1

M:Alternate names: MC033L
C:Species: Molluscum contagiosum virus 1
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C:Accession: T30635
R:Senkevich, T.G.; Bugert, J.J.; Steller, J.R.; Koonin, E.V.; Darai, G.; Moss, B.; Science 273, 813-816, 1996
A:Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host restriction sites
A:Reference number: Z28076; PMID:96325459; PMID:8670425
A:Accession: T30635
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-579 <SEN>
A:Cross-references: UNIPROT:Q98201; EMBL:U60315; NID:g1491943; PIDN:AAC55161.1; PID:g1491943
C:Genetics:
A:Note: MC033L
C:Superfamily: Molluscum contagiosum virus 1 hypothetical protein 33L

Query Match 63.8%; Score 44; DB 2; Length 579;
Best Local Similarity 70.0%; Pred. No. 11;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTGYPEP 10
DB 116 CSSTGYPEP 125

RESULT 6

hypothetical protein B0391.10 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18731
R:Gardner, A.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19012
A:Accession: T18731
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-92 <WIL>
A:Cross-references: UNIPROT:Q62015; EMBL:Z81454; PIDN:CAH03802.1; GSPDB:GN00023; CESP:B0391
A:Experimental source: clone B0391
C:Genetics:
A:Gene: CESP:B0391.10
A:Map position: 5
A:Introns: 18/1

Query Match 60.9%; Score 42; DB 2; Length 92;
Best Local Similarity 70.0%; Pred. No. 3.7;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTGYPEP 10
DB 35 CSSTGYPEP 44

RESULT 7

CD80 precursor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004
C:Accession: 146690
R:Isono, T.; Seto, A.; Immunogenetics 42, 217-220, 1995
A:Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecule CD80 precursor
A:Reference number: 146690; PMID:95369849; PMID:7642234
A:Accession: 146690
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-299 <ISO>
A:Cross-references: UNIPROT:P42070; GB:D49843; NID:g755096; PIDN:BAA08643.1; PID:g755096
C:Superfamily: B-lymphocyte restricted antigen B7

Query Match 60.9%; Score 42; DB 2; Length 299;
 Best Local Similarity 54.5%; Pred. No. 12;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSSTGYPEPQ 11
 ||:|||||
 DB 161 CSASGCFPEPR 171

RESULT 8

butyrophilin - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 15-Mar-2004
 C/Accession: S65133
 R/Joshi, T.; Aoki, N.; Noda, A.; Adachi, T.; Nakamura, R.; Matsuda, T.
 Biochim. Biophys. Acta 1245, 285-292, 1995
 A/Title: Carboxy-terminal cytoplasmic domain of mouse butyrophilin specifically associated
 A/Reference number: S65133; PMID:96125722; PMID:8541302
 A/Accession: S65133
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-487 <ISH>
 A/Cross-references: GB:S60642; NID:G1246078; PID:AA835893.1; PID:G1246079
 C/Superfamily: rfp transforming protein

Query Match 60.9%; Score 42; DB 2; Length 487;
 Best Local Similarity 63.6%; Pred. No. 20;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTGYPEPQ 11
 ||:|||||
 DB 128 CTSAGWPEPQ 138

RESULT 9

A45803
 B-cell-restricted antigen B7 precursor - human
 N/Alternate names: B-lymphocyte activation antigen B7
 C/Species: Homo sapiens (man)
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
 C/Accession: I54495; A45803
 R/Selvakumar, A.; Mohanraj, B.K.; Eddy, R.L.; Shows, T.B.; White, P.C.; Dupont, B.
 Immunogenetics 36, 175-181, 1992
 A/Title: Genomic organization and chromosomal location of the human gene encoding the B-
 A/Reference number: I54495; PMID:92307753; PMID:1177173
 A/Accession: I54495
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-288 <RES>
 R/Freeman, G.J.; Freedman, A.S.; Segal, J.M.; Lee, G.; Whitman, J.F.; Nadler, L.M.
 J. Immunol. 153, 2714-2722, 1995
 A/Title: B7, a new member of the Ig superfamily with unique expression on activated and
 A/Reference number: A45803; MUID:90010147; PMID:2794510
 A/Accession: A45803
 A/Molecule type: mRNA
 A/Residues: 1-288 <PRE>
 A/Cross-references: GB:M27533; NID:G184680; PIDN:AAA36045.1; PID:G306916
 C/Genetics:
 A/Gene: GDB:CD80; CD28LG1; CD28
 A/Cross-references: GDB:251792; OMIM:112203
 A/Map position: 3q13.3-q21
 A/Intons: 34/1; 140/1; 234/1; 266/1
 C/Superfamily: B-lymphocyte restricted antigen B7
 C/Keywords: transmembrane protein
 F:1-26/Domain: signal sequence #status predicted <SIG>
 F:248-264/Domain: transmembrane #status predicted <TM>

Query Match 59.4%; Score 41; DB 2; Length 288;
 Best Local Similarity 60.0%; Pred. No. 17;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSSTGYPEP 10
 ||:|||||
 DB 162 CSTSGCFPEPR 171

RESULT 10

G00031
 B7 protein - red-crowned mangabey (fragment)
 C/Species: Cercopithecus torquatus (red-crowned mangabey, white-collared mangabey)
 C/Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004
 C/Accession: G00031
 R/Villinger, F.J.
 submitted to the EMBL Data Library, January 1995
 A/Reference number: G00217
 A/Accession: G00031
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-289 <VIL>
 A/Cross-references: UNIPROT:Q28347; EMBL:U19833; NID:G644783; PIDN:AAA6700.1; PID:G644
 C/Genetics:
 A/Gene: B7
 C/Superfamily: B-lymphocyte restricted antigen B7

Query Match 59.4%; Score 41; DB 2; Length 289;
 Best Local Similarity 60.0%; Pred. No. 17;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSSTGYPEP 10
 ||:|||||
 DB 162 CSTSGCFPEPR 171

RESULT 11

S70587
 butyrophilin precursor - human
 C/Species: Homo sapiens (man)
 C/Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 C/Accession: S70587
 R/Taylor, M.R.; Peterson, J.A.; Ceriani, R.L.; Couto, J.R.
 Biochim. Biophys. Acta 1306, 1-4, 1996
 A/Title: Cloning and sequence analysis of human butyrophilin reveals a potential receptor
 A/Reference number: S70587; MUID:96201696; PMID:8611614
 A/Accession: S70587
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-526 <TAY>
 A/Cross-references: UNIPROT:Q13410; EMBL:U39576; NID:G1326082; PIDN:AA650489.1; PID:G13
 C/Superfamily: rfp transforming protein

Query Match 59.4%; Score 41; DB 2; Length 526;
 Best Local Similarity 63.6%; Pred. No. 32;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CSSTGYPEPQ 11
 ||:|||||
 DB 164 CTSAGWPEPQ 174

RESULT 12

A37821
 butyrophilin - bovine
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 09-Jul-2004
 C/Accession: A37821
 R/Jack, L.J.W.; Mather, I.H.
 J. Biol. Chem. 265, 14481-14486, 1990
 A/Title: Cloning and analysis of cDNA encoding bovine butyrophilin, an apical glycoprotein
 A/Reference number: A37821; MUID:90354441; PMID:2387867
 A/Accession: A37821
 A/Status: preliminary
 A/Molecule type: mRNA

A:Residues: 1-526 <JAC>
 A:Cross-references: UNIPROT:P18892; GB:M35551; NID:G1763685; PIDN:AAB39766.1; PID:G16277
 C:Superfamily: rfp transforming protein
 C:Keywords: transmembrane protein

Query Match 59.4%; Score 41; DB 2; Length 526;
 Best Local Similarity 63.6%; Pred. No. 32;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CSSTGYPEPQ 11
 |||
 Db 164 CTSVGVWPEPQ 174

RESULT 13

T29549
 hypothetical protein ZK377.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 C:Accession: T29549

R:Nhan, M.; Hawkins, J.

A:Description: The sequence of C. elegans cosmid ZK377.
 submitted to the EMBL Data Library, February 1997

A:Reference number: Z20633

A:Accession: T29549

A:Status: preliminary; translated from GB/EMBL/DDBU

A:Molecule type: DNA

A:Residues: 1-423 <NHA>

A:Cross-references: EMBL:U88183; PIDN:AAB52658.1; GSPDB:GN00028; CESP:ZK377.3

A:Experimental source: strain Bristol N2; clone ZK377

C:Genetics:

A:Gene: CESP:ZK377.3

A:Map position: X

A:introns: 24/1; 142/3; 229/3; 284/2; 408/3

Query Match 58.0%; Score 40; DB 2; Length 423;
 Best Local Similarity 60.0%; Pred. No. 38;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTGYPEPQ 10
 |||
 Db 153 CSPPRGFPEP 162

RESULT 14

T42405
 sax-3 protein - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: T42405

R:Zallen, J.A.; Yi, B.A.; Bargmann, C.I.

Cell 92, 217-227, 1998

A:Title: The conserved immunoglobulin superfamily member SAX-3/Robo directs multiple asp

A:Reference number: Z22160; MUID:98117250; PMID:9458046

A:Accession: T42405

A:Status: preliminary; translated from GB/EMBL/DDBU

A:Molecule type: mRNA

A:Residues: 1-1273 <ZAL>

A:Cross-references: UNIPROT:O44928; EMBL:AF041053; NID:G2804779; PIDN:AAC38848.1; PID:G2

C:Genetics:

A:Note: sax-3

A:Function:

A:Description: sax-3 function is required at the time of axon guidance

Query Match 58.0%; Score 40; DB 2; Length 1273;
 Best Local Similarity 60.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTGYPEPQ 10
 |||
 Db 154 CSPPRGFPEP 163

RESULT 15

C48150
 hibernation-related protein HP-27 precursor - Siberian chipmunk

C:Species: Eutamias sibiricus (Siberian chipmunk)

C>Date: 16-Feb-1994 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C:Accession: C48150; A41752

R:Takanatsu, N.; Ohba, K.; Kondo, J.; Shiba, T.

Mol. Cell. Biol. 13, 1516-1521, 1993

A:Title: Hibernation-associated gene regulation of plasma proteins with a collagen-like

A:Reference number: A48150; MUID:93180798; PMID:8441393

A:Accession: C48150

A:Molecule type: mRNA; protein

A:Residues: 1-215 <TAK>

A:Cross-references: UNIPROT:O06577; GB:D12976; NID:G287471; PIDN:BAO2353.1; PID:G28747

A:Note: the source is designated as Tamias asiaticus in Genbank entry TMSHP27, release

A:Note: sequence extracted from NCBI backbone (NCBIN:125948, NCBI:P:125949)

R:Kondo, N.; Kondo, J.

J. Biol. Chem. 267, 473-478, 1992

A:Title: Identification of novel blood proteins specific for mammalian hibernation.

A:Reference number: A41752; MUID:92112696; PMID:1730610

A:Accession: A41752

A:Status: preliminary

A:Molecule type: protein

A:Residues: 31-40, 'A', 42-50, 'Q', 52-215 <KON>

C:Superfamily: complement subcomponent C1q chain A; complement C1q carboxyl-terminal hot

C:Keywords: glycoprotein; hibernation; plasma

F:1-30/Domain: signal sequence #status predicted <SIG>

F:31-215/Product: hibernation-related protein HP-27 #status experimental <NAT>

F:31-214/Domain: complement C1q carboxyl-terminal homology <CIQ>

F:155/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 56.5%; Score 39; DB 2; Length 215;
 Best Local Similarity 77.8%; Pred. No. 28;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTGYPEPQ 9
 |||
 Db 29 CSSTGQNP 37

..

Search completed: December 15, 2004, 16:38:02
 Job time : 16.2857 sec

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OM protein - protein search, using sw model

Run on: December 15, 2004, 16:24:31 ; Search time 66.2557 Seconds
(without alignments)
104.163 Million cell updates/sec

```
Title: US-09-868-605-14_COPY_151_162
Perfect score: 69
Sequence: 1 CSSTQGYPEPQR 12
```

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Match	Length	DB	ID	Description
1	69	100.0	325	2	002938	002938 sus scrofa
2	63	91.3	284	2	Q9GLJ3	Q9GLJ3 bos taurus
3	57	82.6	330	1	CB86_RABIT	P42071 oryctolagus
4	54	78.3	280	2	Q9TTF1	Q9TTF1 canis familiaris
5	54	78.3	329	2	Q9TTF2	Q9TTF2 canis familiaris
6	54	78.3	329	2	Q9XSX6	Q9XSX6 felis silvestris
7	54	78.3	332	2	Q9GMZ7	Q9GMZ7 felis silvestris
8	54	78.3	332	2	Q9SIL6	Q9SIL6 felis silvestris
9	52	75.4	275	2	Q9BDN9	Q9BDN9 papio anubis
10	52	75.4	323	2	Q9BDN8	Q9BDN8 papio anubis
11	52	75.4	323	2	Q9BDN2	Q9BDN2 ceropithecus
12	52	75.4	323	2	Q9BDW4	Q9BDW4 macaca nemata
13	52	75.4	323	2	Q9BDW9	Q9BDW9 macaca nemata
14	51	73.9	329	1	CB86_HUMAN	P42061 homo sapiens
15	51	73.9	329	2	AAH40261	AAH40261 homo sapiens
16	50	72.5	149	2	Q62810	Q62810 ratus norvegicus
17	50	72.5	313	2	Q35531	Q35531 ratus norvegicus
18	47	68.1	281	2	Q8CJF8	Q8CJF8 mesocricetus
19	46	68.7	316	2	Q8UX12	Q8UX12 homo sapiens
20	46	68.7	316	2	Q7PF84	Q7PF84 ratus norvegicus
21	46	66.7	316	2	Q6VE99	Q6VE99 mus musculus
22	46	66.7	316	2	AAH56608	AAH56608 mus musculus
23	46	66.7	316	2	AAQ88709	AAQ88709 homo sapiens
24	46	66.7	388	2	Q8NC34	Q8NC34 homo sapiens
25	46	66.7	493	2	Q6P5Y4	Q6P5Y4 homo sapiens
26	46	66.7	493	2	AAH62581	AAH62581 homo sapiens
27	46	66.7	533	2	Q8NC86	Q8NC86 homo sapiens
28	46	66.7	534	2	Q8NBI8	Q8NBI8 homo sapiens
29	44	63.8	309	1	CB86_MOUSE	P42092 mus musculus
30	44	63.8	309	2	AAH25680	AAH25680 mus musculus
31	44	63.8	309	2	AAH25681	AAH25681 mus musculus

44	63.8	309	2	AAD25882	Aad25882 mus muscu
33	63.8	309	2	AAD25883	Aad25883 mus muscu
32	63.8	309	2	BAC37666	Bac37666 mus muscu
44	63.8	314	2	Q61238	Q61238 mus muscu
35	63.8	356	2	Q64381	Q64381 mus muscu
36	63.8	379	2	Q98201	Q98201 moluscum g
44	63.8	256	2	Q42404	Q42404 gallus galli
38	62.3	332	1	ICOL_MOUSE	Q31518 mus muscu
39	62.3	332	1	BAC30938	BAC30938 mus muscu
40	62.3	92	2	Q62015	Q62015 caenorhabdi
41	60.9	289	1	CD80_RABIT	Q62005 crotolagu
42	60.9	309	2	Q91YV7	Q91YV7 mus muscu
43	60.9	309	2	Q9EXR1	Q9EXR1 homo sapien
44	60.9	510	2	Q6EH12	Q6EH12 ratu

ID	002838	PRELIMINARY;	PRT;	325 AA.
AC	002838.			
DT	01-JUL-1997	(TREMBLrel. 04, Created)		
DT	01-JUL-1997	(TREMBLrel. 04, Last sequence update)		
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)		
DE	B7-2.			
GN	Name=CD86;			
OS	Sus scrofa (Pig).			
OC	Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;			
OC	Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.			
OX	NCBI_TaxID=9823;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97047772; PubMed=8892613;			
RA	Maier S.E., Karmann K., Min W., Hughes C.C., Pober J.S.,			
RA	Bochwell A.L.;			
RT	"Porcine endothelial CD86 is a major costimulator of xenogeneic human			
RT	T cells: cloning, sequencing, and functional expression in human			
RT	endothelial cells.";			
RL	J. Immunol. 157:3838-3844(1996).			
DR	EMBL; L76099; AAB61307.1; -.			
DR	HSSP; P42081; INCN.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003596; Ig_V.			
DR	Pfam; PF00047; Ig; 1.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS0835; IG Like; 1.			
SQ	SEQUENCE 325 AA; 36527 MW; 988BE08137B0597D CRC64;			
Query Match:		100.0%;	Score 69;	DB 2; Length 325;
Best Local Similarity		100.0%;	Pred. No. 0.00076;	
Matches 12; Conservative		0;	Mismatches 0;	Indels 0; Gaps 0
OY	1	CSSTGYPEPOR 12		
DB	151	CSSTGYPEPOR 162		
RESULT 2				
Q9GLJ3				
ID	Q9GLJ3	PRELIMINARY;	PRT;	284 AA.
AC	Q9GLJ3.			
DT	01-MAR-2001	(TREMBLrel. 16, Created)		
DT	01-MAR-2001	(TREMBLrel. 16, Last sequence update)		
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)		
DE	CD86 antigen (Fragment).			
GN	Name=CD86;			
OS	Bos taurus (Bovine).			
OC	Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;			
OC	Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae;			
OC	Bovinae, Bos			
OX	NCBI_TaxID=9913;			

```

RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=peripheral blood;
RA Brooke G.P., Howard C.J., Parsons K.R.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; A0291475; CAC13140.1; -.
DR InterPro; IPR007110; IG-1-like.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IG_1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 284 AA; 284 AA; 797B8639B297841 CRC64;
SQ SEQUENCE 284 AA; 32021 MW; 797B8639B297841 CRC64;

Query Match
Best Local Similarity 91.3%; Score 63; DB 2; Length 284;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSSTOQYPPRQ 12
DB 165 CSSTOQYPPRQ 176

RESULT 3
CD86 RABIT STANDARD; PRT; 330 AA.
AC P42071;
DT 01-NOV-1995 (rel. 32, Created)
DT 01-NOV-1995 (rel. 32, Last sequence update)
DT 05-JUL-2004 (rel. 44, Last annotation update)
DE B lymphocyte activation antigen CD86 precursor (Activation B7-2
  antigen)
GN Name=CD86;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B/O X CHBR;HM;
RA MEDLINE=95369849; PubMed=7642234;
RX Isono T., Seto A.;
RT "Cloning and sequencing of the rabbit gene encoding T-cell
  costimulatory molecules."
RT Immunogenetics 42:217-220(1995).
CC - FUNCTION: Receptor involved in the costimulatory signal essential
  for T lymphocyte proliferation and interleukin 2 production, by
  binding CD28 or CTLA-4. May play a critical role in the early
  events of T cell activation and costimulation of native T cells,
  such as deciding between immunity and anergy that is made by T
  cells within 24 hours after activation.
CC - SUBCELLULAR LOCATION: Type I membrane protein.
CC - SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC - SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
  use by non-profit institutions as long as its content is in no way
  modified and this statement is not removed. Usage by and for commercial
  entities requires a license agreement (See http://www.isb-sib.ch/announce/
  or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D49842; BAA08642.1; -.
CC PIR; I46591; I46591.
CC HSSP; P42081; INCN.
CC InterPro; IPR007110; IG_1-like.
CC InterPro; IPR003006; IG_MHC.
CC InterPro; IPR003596; IG_V.
CC SMART; SM00406; IG_1.
CC PROSITE; PS00835; IG_LIKE; 1.
CC PROSITE; PS00290; IG_MHC; 1.
KW Glycoprotein; Immunoglobulin domain; Receptor; Signal; T-cell;

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KW Transmembrane.
FT SIGNAL 1 22 Potential.
FT CHAIN 23 330 B lymphocyte activation antigen CD86.
FT DOMAIN 23 247 Extracellular (Potential).
FT TRANSMEM 248 268 Potential.
FT DOMAIN 269 330 Cytoplasmic (Potential).
FT DOMAIN 33 127 Ig-like V-type.
FT DOMAIN 150 225 Ig-like C2-type.
FT DISULFID 40 110 Potential.
FT DISULFID 157 218 Potential.
FT CARBOHYD 133 33 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 135 135 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 146 146 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 154 154 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 177 177 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 192 192 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 198 198 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 213 213 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 330 AA; 37142 MW; 935CDB5C57E3EE1 CRC64;

Query Match
Best Local Similarity 82.6%; Score 57; DB 1; Length 330;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSSTOQYPPRQ 12
DB 157 CSSTOQYPPRQ 168

RESULT 4
O9TTF1 PRELIMINARY; PRT; 280 AA.
AC O9TTF1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Truncated B7-2 protein.
GN Name=CD86;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=2009396; PubMed=10630300;
RX Yang S., Sim G.-K.;
RT "New forms of dog CD80 and CD86 transcripts that encode secreted B7
  molecules."
RT Immunogenetics 50:349-353(1999).
RL EMBL; AF106827; AAF17298.1; -.
DR HSSP; P42081; INCN.
DR InterPro; IPR007110; IG_1-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IG_1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 280 AA; 32265 MW; 3C8BCA4D826A7F3 CRC64;

Query Match
Best Local Similarity 78.3%; Score 54; DB 2; Length 280;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSSTOQYPPRQ 11
DB 158 CSSTOQYPPRQ 168

RESULT 5
O9TTF2 PRELIMINARY; PRT; 329 AA.
AC O9TTF2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)

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01-MAY-2000 (TREMBlrel. 13, last sequence update)
01-MAR-2004 (TREMBlrel. 26, last annotation update)
DE B7-2 protein.
GN Name=CD86;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2009396; PubMed=10630300;
RA Yang S., Sim G.-K.;
RT "New forms of dog CD80 and CD86 transcripts that encode secreted B7
RT molecules."
RL Immunogenetics 50:349-353(1999).
DR EMBL; AF106826; AAF1297.1; -.
DR HSSP; P42081; INCN.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 329 AA; 37774 MW; D9BBB6347BF7B73 CRC64;

Query Match 78.3%; Score 54; DB 2; Length 329;
Best Local Similarity 81.8%; Pred. No. 0.37;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0

QY 1 CSSTQGYPEPQ 11
DB 158 CSSTQGYPEPK 168
ID Q9XSX6 PRELIMINARY; PRT; 329 AA.
Q9XSX6
AC Q9XSX6;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE CD86 antigen.
GN Name=CD86;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20180222; PubMed=10713336;
RA Choi I.-S., Hash S.M., Winslow B.J., Collisson E.M.;
RT "Sequence analyses of feline B7 costimulatory molecules."
RT Ver. Immunol. Immunopathol. 73:219-231(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Choi I.-S., Hash S., Winslow B.J., Collisson E.M.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF157827; AAD42974.1; -.
DR HSSP; P42081; INCN.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
SQ SEQUENCE 329 AA; 37481 MW; A10621B3C00A08BB CRC64;

Query Match 78.3%; Score 54; Length 329;
Best Local Similarity 81.8%; Pred. No. 0.37;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0

QY 1 CSSTQGYPEPQ 11
DB 159 CSSTQGYPEPK 169

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RESULT 7
ID 09GMZ7 PRELIMINARY; PRT; 332 AA.
AC 09GMZ7;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE B-lymphocyte activation antigen B7-2 (CD86).
GN Name=CD86;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
CX NCB1_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2048532; PubMed=11029611;
RA Nishimura Y., Shimojima M., Miyazawa T., Sato E., Nakamura K.,
RA Izumiya Y., Ikeda Y., Mikami T., Takahashi E.;
RT "Molecular cloning of the cDNA encoding the feline B-lymphocyte
RT activation antigen B7-1 (CD80) and B7-2 (CD86) homologues which
RT interact with human CTLA4-19."
RL Eur. J. Immunogenet. 27:427-430(2000).
DR HSSP; P42081; INCN.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_V.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PSS0835; IG LIKE; 1.
SO SEQUENCE 332 AA; 37812 MW; 672C8B3667D1E3C0 CRC64;

Query Match 78.3%; Score 54; DB 2; Length 332;
Best Local Similarity 81.8%; Pred. No. 0.38;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0.

CY 1 CSSTQGYPEPO 11
Db 159 CSSTQGYPEPK 169
|||||
|

RESULT 8
ID 09SL16 PRELIMINARY; PRT; 332 AA.
AC 09SL16;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE CD86.
GN Name=CD86;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
CX NCB1_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21390213; PubMed=11496243;
RA Yang S., Sellins K.S., Powell T., Stoneman E., Sim G.K.;
RT "Novel transcripts encoding secreted forms of feline CD80 and CD86
RT costimulatory molecules."
RL Vet. Immunol. Immunopathol. 81:15-21(2001).
DR EMBL; AY007704; AAG33342.1; -.
DR HSSP; P42081; INCN.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_V.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PSS0835; IG LIKE; 1.
SO SEQUENCE 332 AA; 37826 MW; 8BFC8B3667D1E3D8 CRC64;

Query Match 78.3%; Score 54; DB 2; Length 332;
Best Local Similarity 81.8%; Pred. No. 0.38;
Matches 9; Conservative 1; Mismatches 0; Gaps 0

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Db 159 CSSTGYPEPCK 169

RESULT 9

Q9BDN9 PRELIMINARY; PRT; 275 AA.

AC Q9BDN9; 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE CD86 protein precursor.

OS Papio anubis (Olive baboon).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC NCBI_TaxID=9555; IG_LIKE; 1.

RP SEQUENCE FROM N.A.

RX MEDLINE=21383618; PubMed=11491535;

RA Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,

Weiss W.R., Ansari A.A.,

"Cloning, sequencing, and homology analysis of nonhuman primate

Fas/Fas-ligand and co-stimulatory molecules.";

RL Immunogenetics 53:315-328(2001).

DR EMBL; AF344836; AAK37532.1; -.

DR HSSP; P42081; INCN.

DR InterPro; IPR007110; IG-like.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

KW SIGNAL.

FT SIGNAL.

SQ SEQUENCE 275 AA; 31343 MW; 3AAD3481B4F37C19 CRC64;

Query Match

Best Local Similarity 75.4%; Score 52; DB 2; Length 275;

Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTGYPEPCK 12

Db 151 CSSTGYPEPCK 162

RESULT 10

Q9BDN9 PRELIMINARY; PRT; 323 AA.

AC Q9BDN9; 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE CD86 protein precursor.

OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecoidea; Cercopithecus.

OC NCBI_TaxID=9531; IG_LIKE; 1.

RP SEQUENCE FROM N.A.

RX MEDLINE=21383618; PubMed=11491535;

RA Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,

Weiss W.R., Ansari A.A.,

"Cloning, sequencing, and homology analysis of nonhuman primate

Fas/Fas-ligand and co-stimulatory molecules.";

RL Immunogenetics 53:315-328(2001).

DR EMBL; AF344840; AAK37536.1; -.

DR HSSP; P42081; INCN.

DR GO; GO:0016021; C:integral to membrane; ISS.

DR GO; GO:0015026; F:coreceptor activity; ISS.

DR GO; GO:0005515; F:protein binding; ISS.

DR GO; GO:0016563; F:transcriptional activator activity; ISS.

DR GO; GO:0007267; P:cell-cell signaling; ISS.

DR GO; GO:0045086; P:positive regulation of interleukin-2 biosyn. . .; ISS.

DR GO; GO:0045086; P:positive regulation of interleukin-4 biosyn. . .; ISS.

DR GO; GO:0045630; P:positive regulation of T-helper 2 cell diff. . .; ISS.

DR GO; GO:0045941; P:positive regulation of transcription; ISS.

DR GO; GO:0043017; P:positive regulation of tumor necrosis facto. . .; ISS.

DR GO; GO:0042110; P:T-cell activation; ISS.

DR InterPro; IPR007110; IG-like.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

DR SIGNAL.

DR SIGNAL.

FT CHAIN 17 323

SQ SEQUENCE 323 AA; 37010 MW; 45B217606A79B75 CRC64;

Query Match

Best Local Similarity 75.4%; Score 52; DB 2; Length 323;

Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTGYPEPCK 12

Db 151 CSSTGYPEPCK 162

RESULT 11

Q9BDM2 PRELIMINARY; PRT; 323 AA.

AC Q9BDM2; 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE CD86 protein.

OS Cercopithecus aethiops (Green monkey) (Grivet).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecoidea; Cercopithecus.

OC NCBI_TaxID=9534; IG_LIKE; 1.

RP SEQUENCE FROM N.A.

RX MEDLINE=21383618; PubMed=11491535;

RA Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,

Weiss W.R., Ansari A.A.,

"Cloning, sequencing, and homology analysis of nonhuman primate

Fas/Fas-ligand and co-stimulatory molecules.";

RL Immunogenetics 53:315-328(2001).

DR EMBL; AF344861; AAK37543.1; -.

DR HSSP; P42081; INCN.

DR GO; GO:0016021; C:integral to membrane; ISS.

DR GO; GO:0015026; F:coreceptor activity; ISS.

DR GO; GO:0005515; F:protein binding; ISS.

DR GO; GO:0016563; F:transcriptional activator activity; ISS.

DR GO; GO:0045086; P:positive regulation of interleukin-2 biosyn. . .; ISS.

DR GO; GO:0045630; P:positive regulation of T-helper 2 cell diff. . .; ISS.

DR GO; GO:0045941; P:positive regulation of transcription; ISS.

DR GO; GO:0043017; P:positive regulation of tumor necrosis facto. . .; ISS.

DR GO; GO:0042110; P:T-cell activation; ISS.

DR InterPro; IPR007110; IG-like.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

SQ SEQUENCE 323 AA; 37045 MW; 3E43152A8ED17267 CRC64;

Query Match

Best Local Similarity 75.4%; Score 52; DB 2; Length 323;

Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTGYPEPCK 12

Db 151 CSSTGYPEPCK 162

RESULT 12

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Q9BDM4          PRELIMINARY;      PRT;      323 AA.
ID Q9BDM4
AC Q9BDM4;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE CD86 protein precursor.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
NCBI_TaxID=9544;
OX
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21383618; PubMed=11491535;
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-ligand and co-stimulatory molecules.";
RT Immunogenetics 53:315-328(2001).
RL EMBL; AF344857; AAK37540.1; -.
DR HSSP; P42081; INCN.
DR GO; GO:0016021; C:integral to membrane; ISS.
DR GO; GO:0015026; F:coreceptor activity; ISS.
DR GO; GO:0005515; F:protein binding; ISS.
DR GO; GO:0016563; F:transcriptional activator activity; ISS.
DR GO; GO:0007267; P:cell-cell signaling; ISS.
DR GO; GO:0045086; P:positive regulation of interleukin-2 biosyn. . .; ISS.
DR GO; GO:0045404; P:positive regulation of interleukin-4 biosyn. . .; ISS.
DR GO; GO:0045630; P:positive regulation of T-helper 2 cell diff. . .; ISS.
DR GO; GO:0045941; P:positive regulation of transcription; ISS.
DR GO; GO:0043017; P:positive regulation of tumor necrosis facto. . .; ISS.
DR GO; GO:0042110; P:T-cell activation; ISS.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM SIGNAL.
FT SIGNAL.
SQ SEQUENCE 323 AA; 37019 MW; D21E103DB1A7D7A CRC64;

Query Match          75.4%; Score 52; DB 2; Length 323;
Best Local Similarity 66.7%; Pred. NO. 0.83;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTQGYPEPQR 12
DB 151 CSSTHGYPEPEK 162

RESULT 13
Q9BDM9          PRELIMINARY;      PRT;      323 AA.
ID Q9BDM9
AC Q9BDM9;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE CD86 protein precursor.
OS Macaca nemestrina (pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
NCBI_TaxID=9545;
OX
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21383618; PubMed=11491535;
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-ligand and co-stimulatory molecules.";
RT Immunogenetics 53:315-328(2001).
RL EMBL; AF344851; AAK37611.1; -.
DR HSSP; P42081; INCN.

QY 1 CSSTQGYPEPQR 12
DB 151 CSSTHGYPEPEK 162

RESULT 14
CD86_HUMAN      STANDARD;          PRT;      329 AA.
ID CD86_HUMAN
AC P42081; Q13655; Q7M415;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE T lymphocyte activation antigen CD86 precursor (Activation B7-2
DE antigen) (CTLA-4 counter-receptor B7.2) (B70) (FUN-1) (B053).
GN Name=CD86; Synonyms=CD28LG2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=94053735; PubMed=7694363;
RA Freeman G.J., Gribben J.G., Boussiotis V.A., Ng J.W.,
RA Restivo V.A., Jr., Lombard L.A., Gray G.S., Nadler L.M.;
RT "Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human T
RT cell proliferation."
RL Science 262:909-911(1993).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=21092744; PubMed=1162656; DOI=10.1006/birc.2000.4102;
RA Magistrelli G., Caron G., Gauchat J.F., Jeannin P., Bonnefoy Y.,
RA Delneste Y.;
RT "Identification of an alternatively spliced variant of human CD86
RL mRNAs."
RN [3]
RP SEQUENCE OF 7-329 FROM N.A. (ISOFORM 1).
RX MEDLINE=94050123; PubMed=7694153;
RA Azuma M., Ito D., Yagita K., Okumura K., Phillips J.H., Lanier L.L.,
RA Somaza C.;
RT "B70 antigen is a second ligand for CTLA-4 and CD28."
RL Nature 366:76-79(1993).
RN [4]
RP SEQUENCE OF 7-329 FROM N.A. (ISOFORM 1).
RX TISSUE=ForeSkin;
RL MEDLINE=95331831; PubMed=7541777;
RA Tellis C.L., Wang S.S., Renner P., Borriello F., Sharpe A.H.,
RA Green N.R., Gray G.S.;
RT "Genomic organization of the gene coding for the costimulatory human
RT B-lymphocyte antigen B7-2 (CD86).";

```

Immunogenetics 42:85-89(1995).

[5]

CHARACTERIZATION.

MEDLINE=95088403; PubMed=7527824;

Lanier L.V., O'Fallon S., Somosa C., Phillips J.H., Linsley P.S., Okumura K., Ito D., Azuma M.,

CD80 (B7) and CD86 (B70) provide similar costimulatory signals for T cell proliferation, cytokine production, and generation of CTL.",

J. Immunol. 154:97-105(1995).

[6]

IDENTIFICATION AS CD86.

MEDLINE=94348060; PubMed=7520767;

Engel P., Gribben D.G., Freeman G.J., Zhou L.J., Nozawa Y., Abe M., Nadler L.M., Wakasa H., Tedder T.F.;

"The B7-2 (B70) costimulatory molecule expressed by monocytes and activated B lymphocytes is the CD86 differentiation antigen.",

Blood 84:1402-1407(1994).

- FUNCTION: Receptor involved in the costimulatory signal essential for T lymphocyte proliferation and interleukin 2 production, by binding CD28 or CTLA-4. May play a critical role in the early events of T cell activation and costimulation of naive T cells, such as deciding between immunity and anergy that is made by T cells within 24 hours after activation. Isoform 2 interferes with the formation of CD86 clusters, and thus acts as a negative regulator of T cell activation.

- SUBCELLULAR LOCATION: Type I membrane protein.

- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2;

Name=1;

IsoId=PA2081-1; Sequence=Displayed;

Name=2; Synonyms=CD86 deltaEC;

IsoId=PA2081-2; Sequence=VSP 009125;

- TISSUE SPECIFICITY: Expressed by activated B lymphocytes and monocytes.

- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.

- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.

- DATABASE: NAME=PROW; NOTE=CD guide CD86 entry;

WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd86.htm".

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EMBL, L25259; AA58389.1; -

EMBL, U04343; AAB03814.1; -

EMBL, U17722; AA86473.1; -

EMBL, U17717; AA86473.1; JOINED.

EMBL, U17718; AA86473.1; JOINED.

EMBL, U17719; AA86473.1; JOINED.

EMBL, U17721; AA86473.1; JOINED.

PIR, A48754; A48754.

PIR, JCT605; JCT605.

PDB, 1I85; X-ray; A/B=25-134.

PDB, INCN; X-ray; A/B=25-134.

GeneW; HGNC:1705; CD86.

MM: 601020; -

GO: GO:0016021; C: integral to membrane, IC.

GO: GO:0015026; F: coreceptor activity, NAS.

GO: GO:0005515; F: protein binding, IPI.

GO: GO:0016563; F: transcriptional activator activity, NAS.

GO: GO:0007267; P: cell-cell signaling, IC.

GO: GO:0006955; P: immune response, TNS.

GO: GO:0006284; P: positive regulation of cell proliferation, TNS.

GO: GO:0045086; P: positive regulation of interleukin-2 biosyn. . . ; NAS.

GO: GO:0045404; P: positive regulation of interleukin-4 biosyn. . . ; NAS.

GO: GO:0045630; P: positive regulation of T-helper 2 cell diff. . . ; NAS.

GO: GO:0045941; P: positive regulation of transcription, NAS.

GO: GO:0043017; P: positive regulation of tumor necrosis facto. . . ; NAS.

GO: GO:0042110; P: T-cell activation, IC.

InterPro: IPR007110; Ig-like.

InterPro: IPR003006; Ig MHC.

PROSITE: PS50835; IG_LIKE; 1.

PROSITE: PS00290; IG_MHC; PALS3_NEG.

3D-structure; Alternative splicing; Glycoprotein; Immunoglobulin domain; Polymorphism; Receptor; Signal; T-cell; Transmembrane.

KW Transmembrane.

FT SIGNAL 1 23

FT CHAIN 24 329

FT DOMAIN 24 247

FT TRANSMEM 248 268

FT DOMAIN 269 329

FT DOMAIN 33 131

FT DOMAIN 150 225

FT DISULFID 40 110

FT DISULFID 157 218

FT CARBOHYD 33 33

FT CARBOHYD 47 47

FT CARBOHYD 135 135

FT CARBOHYD 146 146

FT CARBOHYD 154 154

FT CARBOHYD 177 177

FT CARBOHYD 192 192

FT CARBOHYD 213 213

FT VARSPLIC 22 234

FT VARIANT 310 310

FT CONFLICT 27 27

FT STRAND 27 31

FT TURN 32 33

FT STRAND 36 37

FT TURN 50 51

FT STRAND 54 58

FT TURN 60 61

FT STRAND 64 69

FT TURN 70 71

FT STRAND 72 73

FT TURN 76 77

FT TURN 80 84

FT STRAND 86 89

FT TURN 90 93

FT STRAND 94 97

FT STRAND 107 113

FT STRAND 122 133

SEQ SEQUENCE 329 AA; 37696 MW; 65D4F3826889CF7D CRC64;

Query Match 73.9%; Score 51; DB 1; Length 329;

Best Local Similarity 66.7%; Pred. No. 1.3;

Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSSTGYPPPPQR 12

Db 157 CSIRHGYPPPK 168

RESULT 15

AAH40261 PRELIMINARY; PRT; 329 AA.

AC AAH40261;

DT 02-VAR-2004 (TREMBLrel. 27, Created)

DT 02-VAR-2004 (TREMBLrel. 27, Last sequence update)

DT 02-VAR-2004 (TREMBLrel. 27, Last annotation update)

DE CD86 antigen, isoform 1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primata; Catarrhini; Hominiidae; Homo.

OX NCBI_TaxID=9606;

RN (1) -

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.C.,

Thu Dec 16 12:21:13 2004

us-09-868-605-14_copy_151_162.rup

Page 7

RA Klausner R.D., Collins F.S., Wagner J., Shermen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buecaw K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.U., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.U.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (NOV--2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC040261; AA040261.1; -; 65DAF3996939CF7D CRC64;
SQ SEQUENCE 329 AA; 37726 MW; 65DAF3996939CF7D CRC64;

Query Match 73.9%; Score 51; DB 2; Length 329;
Best Local Similarity 66.7%; Pred. No. 1.3;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

CY 1 CSSTGYPEPQR 12
|||
Db 157 CSIHGYPEPK 168
|||
|||

Search completed: December 15, 2004, 16:33:38
Job time : 68.2857 secs

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CC human T cells, with particular importance in the context of
 CC xenotransplantation of porcine organs. Recipients are immunised with
 CC hybrid synthetic peptides comprising a T cell epitope conjugated to
 CC sequences of the porcine costimulatory molecules CD80, CD86 or CD40 (see
 CC AA95321-24). Peptides that induce antibodies specific for regions of
 CC costimulatory molecules involved in binding to their counter-receptors on
 CC human cells (CD28 and CD14) are capable of blocking the delivery of
 CC costimulation. Once the antibody response has been induced, the
 CC transplanted organ will recall this response due to the expression of the
 CC costimulatory molecules, thereby sustaining the response, and providing
 CC an endogenous mechanism of costimulatory blockade. The method is useful
 CC for improving the tolerance of a host to xenografts, particularly porcine
 CC pancreatic islet cells

XX Sequence 325 AA;

Query Match 98.5%; Score 325; DB 3; Length 325;
 Best Local Similarity 100.0%; Pred. No. 3.5e-306;
 Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSNILFVWVLLSGAASLKSOAYFNETGELPCHFTNSQNLSDLELVIFWQDDNVLVY 60
 DB 1 MGLSNILFVWVLLSGAASLKSOAYFNETGELPCHFTNSQNLSDLELVIFWQDDNVLVY 60
 QY 61 ELYRGOEKPHNVNSKVMGRISFDQATWTLRLAHNVQIKDKGSYOCFIHHKPGHGLVPIHOM 120
 DB 61 ELYRGOEKPHNVNSKVMGRISFDQATWTLRLAHNVQIKDKGSYOCFIHHKPGHGLVPIHOM 120
 QY 121 SSDLSILANFSPPEINILNHTENSVINLTCSSTOGYEPQPMYMLINTKNSSTTEHDADM 180
 DB 121 SSDLSILANFSPPEINILNHTENSVINLTCSSTOGYEPQPMYMLINTKNSSTTEHDADM 180
 QY 181 KKSQNNITELYNVNSIRVSLPIPETNVSIVCVQLQEPSEKTLFSLPCNIDAKPPVQPPVP 240
 DB 181 KKSQNNITELYNVNSIRVSLPIPETNVSIVCVQLQEPSEKTLFSLPCNIDAKPPVQPPVP 240
 QY 241 DHILMIALLVTVVVCGWVSFVTLRKRKKQPGPSNECGEITIKMRKASEQTNRAREVH 300
 DB 241 DHILMIALLVTVVVCGWVSFVTLRKRKKQPGPSNECGEITIKMRKASEQTNRAREVH 300
 QY 301 ERSDDACQDVNIIKTSADNSTTDF 325
 DB 301 ERSDDACQDVNIIKTSADNSTTDF 325

RESULT 2
 AA95321

ID AA95321 standard; protein; 325 AA.

XX AA95321;

DT 25-SEP-2000 (first entry)

DE Pig costimulatory molecule CD86 (B7-2).

KW Co-stimulatory molecule; CD86, B7-2; pig; immunosuppressive;
 KW xenotransplantation; organ transplant; vaccine; epitope.

XX Sus scrofa.

XX Key Location/Qualifiers

FT Peptide 17..29

FT Peptide /note= "peptide 9"

FT Peptide 21..32 "peptide 8"

FT Peptide /note= "peptide 8"

FT Peptide /note= "peptide 2"

FT Peptide /note= "peptide 10"

FT Peptide /note= "peptide 1"

FT Peptide /note= "peptide 5"

FT Peptide 109..121
 FT /note= "peptide 3"
 FT Peptide 113..121
 FT /note= "peptide 4"
 FT Peptide 151..162
 FT /note= "peptide 6"

PN WO200037102-A2.

XX 29-JUN-2000.

PR 17-DEC-1999; 99WO-GB004200.

XX 19-DEC-1998; 98GB-00027921.

PR 23-OCT-1999; 99GB-00025015.

XX (MML-) ML LAB PLC.

PI Lechler RI, Rogers NJ, Dorling A;

DR WPI; 2000-442537/38.

XX N-PSDB; AAA49661.

PS Disclosure, Fig 6; 81pp; English.

The present sequence is that of pig co-stimulatory molecule CD86 (B7-2),
 as deduced from an isolated cDNA clone (see AA49661). CD86 plays a key
 role in T cell costimulation. The invention relates to a novel strategy
 for inhibiting costimulation by porcine cells of human T cells, with
 particular importance in the context of xenotransplantation of porcine
 organs. Recipients are immunised with hybrid synthetic peptides
 comprising a T cell epitope conjugated to sequences of the porcine
 costimulatory molecules CD80, CD86 or CD40, such as peptides 1-10 of CD86
 (see also AA95325-33). Peptides that induce antibodies specific for
 regions of costimulatory molecules involved in binding to their counter-
 receptors on human cells (CD28 and CD14) are capable of blocking the
 delivery of costimulation. Once the antibody response has been induced,
 the transplanted organ will recall this response due to the expression of
 the costimulatory molecules, thereby sustaining the response, and
 providing an endogenous mechanism of costimulatory blockade. The method
 is useful for improving the tolerance of a host to xenografts,
 particularly porcine pancreatic islet cells

XX Sequence 325 AA;

Query Match 67.9%; Score 224; DB 3; Length 325;
 Best Local Similarity 99.7%; Pred. No. 2.9e-208;
 Matches 324; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGLSNILFVWVLLSGAASLKSOAYFNETGELPCHFTNSQNLSDLELVIFWQDDNVLVY 60
 DB 1 MGLSNILFVWVLLSGAASLKSOAYFNETGELPCHFTNSQNLSDLELVIFWQDDNVLVY 60
 QY 61 ELYRGOEKPHNVNSKVMGRISFDQATWTLRLAHNVQIKDKGSYOCFIHHKPGHGLVPIHOM 120
 DB 61 ELYRGOEKPHNVNSKVMGRISFDQATWTLRLAHNVQIKDKGSYOCFIHHKPGHGLVPIHOM 120
 QY 121 SSDLSILANFSPPEINILNHTENSVINLTCSSTOGYEPQPMYMLINTKNSSTTEHDADM 180
 DB 121 SSDLSILANFSPPEINILNHTENSVINLTCSSTOGYEPQPMYMLINTKNSSTTEHDADM 180
 QY 181 KKSQNNITELYNVNSIRVSLPIPETNVSIVCVQLQEPSEKTLFSLPCNIDAKPPVQPPVP 240
 DB 181 KKSQNNITELYNVNSIRVSLPIPETNVSIVCVQLQEPSEKTLFSLPCNIDAKPPVQPPVP 240
 QY 241 DHILMIALLVTVVVCGWVSFVTLRKRKKQPGPSNECGEITIKMRKASEQTNRAREVH 300
 DB 241 DHILMIALLVTVVVCGWVSFVTLRKRKKQPGPSNECGEITIKMRKASEQTNRAREVH 300
 QY 301 ERSDDACQDVNIIKTSADNSTTDF 325

Db 301 ERSDDAQCDVNIKTASDNDSTTDF 325

RESULT 3

ID AAM14944 standard; protein; 250 AA.

AC AAM14944;

DT 17-OCT-2003 (revised)

DT 16-JUN-1997 (first entry)

DE Chimeric human/porcine CD86.

KM Xenotransplantation; graft rejection; cell interaction; pig; CD86;

KM monoclonal antibody; chimeric antibody; diagnosis.

OS Homo; sapiens.

OS Sus scrofa.

OS Chimeric.

PH Key Location/Qualifiers

FT Peptide 1..25 /label= Sig_peptide

FT Protein 26..250 /label= Mac_protein

FT Region 246..250 /label= Histidine_tag

FT WO9711971-A1.

PD 03-APR-1997.

PF 27-SEP-1996; 96WO-US015575.

PR 28-SEP-1995; 95US-0004489P.

PR 26-SEP-1996; 96US-00004489.

PA (ALEX-) ALEXION PHARM INC.

PI Mueller JP, Evans MJ, Mueller EE, Rollins S, Rother RP, Mattis LA;

DR WPI; 1997-212855/19.

DR N-PSDB; AAT62939.

XX Antibodies binding to porcine but not human cell interaction proteins -

PT useful to treat and assay for rejection of xenografted porcine organs,

PT tissues or cells.

PS Disclosure; Page 69-70; 105pp; English.

XX A chimeric human/porcine CD86 (B7-2) cell adhesion molecule has amino

CC acid residues 1-4 and 197-245 from human CD86, and amino acids 5-196 from

CC porcine CD86. It is encoded by a DNA construct (AAT62939) obtd. by PCR

CC amplification of porcine sequences and ligation to a sequence encoding

CC the C-terminal region of human CD86 Igc domain. A signal sequence

CC facilitates efficient secretion from transfected mammalian cells.

CC Antibodies to porcine CD86 protein, P-selectin (see also AAM14945) and

CC vascular cell adhesion molecule (see also AAM14931-42) are useful for

CC diagnosing human rejection of porcine xenotransplants and for improving

CC xenotransplantation of porcine cells, tissues and organs into human

CC recipients. (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 250 AA;

Query Match 23.0%; Score 76; DB 2; Length 250;

Best Local Similarity 100.0%; Pred. No. 6.8e-65;

Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 FWODDNLVLYELVYRGOKPHNNNSKYMGRTSFOATLTLPLHNVQIKDGSYCCFTHHK 109

DB 56 FWODDNLVLYELVYRGOKPHNNNSKYMGRTSFOATLTLPLHNVQIKDGSYCCFTHHK 115

QY 110 GPHGLVPIHOMSSDLS 125
DB 116 GPHGLVPIHOMSSDLS 131

RESULT 4

ID AAY32278 standard; protein; 329 AA.

AC AAY32278;

DT 12-SEP-2003 (revised)

DT 15-FEB-2000 (first entry)

DE Cat CD86 (B7-2) ligand.

KM CD86; B7-2; ligand; cat; vaccine; feline immunodeficiency virus; FIV;

KM feline leukaemia virus; feline infectious peritonitis virus;

KM feline panleukopaemia virus; feline calicivirus; feline reovirus-3;

KM feline rotavirus; feline coronavirus; feline syncytial virus;

KM feline sarcoma virus; feline herpesvirus; feline Borna disease;

KM rabies virus; chlamydia; Toxoplasmosis gondii; Dirofilaria immitis;

KM parasite; autoimmune disease; transplant rejection; therapy.

XX Felis catus.

XX WO9957271-A2.

XX 11-NOV-1999.

XX 30-APR-1999; 99WO-US009502.

XX 01-MAY-1998; 98US-00071699.

XX (TEXA) TEXAS A & M SYSTEM.

XX Collison EW, Haeh SM, Choi I;

XX WPI; 2000-052972/04.

XX N-PSDB; AAZ34785.

XX Novel feline proteins used to produce feline vaccines which prevent

PT infectious disease or to promote growth in homologous or heterologous

PT species.

PS Example 1A; Fig 3A; 186pp; English.

XX The present sequence represents feline CD86 (B7-2) ligand, as predicted

CC from isolated cDNA of peripheral blood mononuclear cells. The

CC coexpression of CD86 with the costimulatory molecule CD28 (see AAY32279)

CC and a tumour antigen or an antigen from a pathogenic organism has the

CC ability to activate or enhance activation of T-lymphocytes. Coexpression

CC of CD86 with CTLA-4 (see AAY32280) has the ability to regulate activation

CC of T-lymphocytes. The invention provides isolated nucleic acids encoding

CC feline CD86 ligand, feline CD80 (B7-1) ligand, feline CD28 receptor or

CC feline CTLA-4 (CD152) receptor, as well as vectors comprising the nucleic

CC acids, and polypeptides encoded by the nucleic acids. It also provides

CC vaccines comprising the CD86, CD86, CD28 or CTLA-4 polypeptides and

CC further comprising immunogens derived from pathogens, especially feline

CC immunodeficiency virus (FIV), feline leukaemia virus, feline infectious

CC peritonitis virus, feline panleukopaemia virus, feline calicivirus,

CC feline reovirus-3, feline rotavirus, feline coronavirus, feline syncytial

CC virus, feline sarcoma virus, feline herpesvirus, feline Borna disease

CC immitis, or a flag, bacterial pathogen, or parasite (all claimed).

CC vaccines capable of enhancing an immune response, and vaccines capable of

CC suppressing an immune response (suitable for treating an autoimmune

CC disease or tissue or organ transplant rejection) are claimed. (Updated on

CC 12-SEP-2003 to standardise OS field)

XX Sequence 329 AA;

Query Match 4.2%; Score 14; DB 3; Length 329;
 Best Local Similarity 100.0%; Pred. No. 0.00011;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 WTRLHNVOIKDKG 100
 |||||
 DB 94 WTRLHNVOIKDKG 107

RESULT 5
 ID AAY32285
 AAAY32285 standard; protein; 329 AA.
 XX
 AC AAY32285;
 XX
 DT 12-SEP-2003 (revised)
 DT 28-FEB-2000 (first entry)
 XX
 DE Feline CD86 (B7-2).
 XX
 KM CD86; B7-2; feline; cat; recombinant virus; vaccine; immunomodulator;
 KM tumour; cancer; therapy.
 XX
 OS Feline catus.
 XX
 PN MO957295-A1.
 XX
 PD 11-NOV-1999.
 XX
 PF 30-APR-1999; 99WO-US009504.
 XX
 PR 01-MAY-1998; 98US-00071711.
 XX
 PA (SCHE) SCHERING-PLOUGH LTD.
 PA (SCHE) SCHERING-PLOUGH VETERINARY CORP.
 XX
 PI Winslow BJ, Cochran MD;
 XX
 DR WPI; 2000-062155/05.
 DR N-PSDB; AA34838.
 XX
 PT Novel recombinant virus useful as immunomodulators, particularly in
 PT vaccines.
 XX
 PS Disclosure; Fig 3A; 230pp; English.
 XX
 CC This sequence represents feline CD86 (B7-2), as deduced from peripheral
 CC blood mononuclear cell cDNA (see AA34838). Manipulating the expression
 CC of CD28 or CTLA-4 (and/or their co-stimulatory ligands CD80 and CD86)
 CC regulates T cell proliferation and cytokine release. The invention
 CC relates to a recombinant virus that contains at least one foreign nucleic
 CC acid, inserted into a nonessential genomic region, that encodes feline
 CC CD28, CD80, CD86 or CTLA-4 protein, or their immunogenic fragments, and
 CC is expressed when the recombinant virus is introduced into a suitable
 CC host. The invention also provides: a recombinant virus further comprising
 CC a foreign nucleic acid encoding an immunogen derived from a feline
 CC pathogen; recombinant viruses capable of enhancing an immune response to
 CC protect against disease; recombinant viruses expressing antisense
 CC sequences, capable of suppressing an immune response in a feline, e.g.
 CC for treatment of autoimmune disease or transplant rejection; and
 CC recombinant viruses expressing DNA encoding CD80 and/or CD86 used to
 CC reduce or eliminate a tumour in cats. (Updated on 12-SEP-2003 to
 CC standardise OS field)
 XX
 SQ Sequence 329 AA;

Query Match 4.2%; Score 14; DB 3; Length 329;
 Best Local Similarity 100.0%; Pred. No. 0.00011;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 WTRLHNVOIKDKG 100
 |||||
 DB 94 WTRLHNVOIKDKG 107

RESULT 6
 ID AA017734
 AA017734 standard; protein; 329 AA.
 XX
 AC AA017734;
 XX
 DT 08-AUG-2002 (first entry)
 XX
 DE Feline CD86.
 XX

KM Cat; CD28; CTLA-4; CD86; immunogen; vaccine; viral infection;
 KM feline immunodeficiency disease; feline infectious peritonitis;
 KM feline leukaemia virus; cancer; degenerative disease; autoimmune disease;
 KM viricide; immunomodulator; cytostatic; immunodeficiency.
 XX
 OS Feline catus.
 XX
 PN US2002051792-A1.
 XX
 PD 02-MAY-2002.
 XX
 PF 30-APR-1999; 99US-00303040.
 XX
 PR 01-MAY-1998; 98US-0083870P.
 XX
 PA (WINS/) WINSLOW B J.
 PA (COCH/) COCHRAN M D.
 XX
 PI Winslow BJ, Cochran MD;
 XX
 DR WPI; 2002-415200/44.
 DR N-PSDB; AA46840.
 XX
 PT New recombinant virus, useful for immunizing felines to prevent or treat
 PT feline immunodeficiency virus, comprises foreign nucleic acid encoding
 PT feline cytotoxic T lymphocyte accessory molecules CD28, CD80, CD86 or
 PT CTLA-4.
 XX
 PS Disclosure; Fig 3; 77pp; English.
 XX
 CC The present invention relates to a recombinant virus comprising at least
 CC one foreign nucleic acid encoding a protein selected from feline
 CC cytotoxic T lymphocyte accessory molecules CD28, CD80, CD86 or CTLA-4,
 CC which is capable of expression when the virus is introduced into an
 CC appropriate host. The virus can be administered to the feline in order to
 CC elicit or enhance an immune response to prevent or treat feline
 CC immunodeficiency disease, feline leukaemia, feline infectious peritonitis,
 CC cancers, degenerative and autoimmune diseases and immunodeficiency. The
 CC present sequence is a cytotoxic T lymphocyte accessory molecule described
 CC in the exemplification of the invention
 XX
 SQ Sequence 329 AA;

Query Match 4.2%; Score 14; DB 5; Length 329;
 Best Local Similarity 100.0%; Pred. No. 0.00011;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 WTRLHNVOIKDKG 100
 |||||
 DB 94 WTRLHNVOIKDKG 107

RESULT 7
 ID AAU78121
 AAU78121 standard; protein; 329 AA.
 XX
 AC AAU78121;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE Feline CD86 protein.
 XX

XX Cat; vaccine; feline immunodeficiency virus; FIV; immunosuppressant;
 KM feline infectious peritonitis; CD80 ligand; CD86 ligand; CD28; receptor;
 KM CTLA-4; vaccine; rabies; autoimmune disease; organ transplant; feline leukemia;
 KM toxoplasmosis gondii; flea; parasite; panleukopenia; feline leukemia;
 KM FelV; calicivirus; rotavirus; reovirus type 3; coronavirus; herpes;
 KM borna disease.
 XX
 OS Felis sp.
 XX
 XX US2002028208-A1.
 XX
 XX 07-MAR-2002.
 XX
 XX 30-APR-1999; 99US-00303510.
 XX
 XX 01-MAY-1998; 98US-0083669P.
 XX
 XX (COLL/) COLLISON E W.
 XX (HASH/) HASH S M.
 XX (CHOI/) CHOI I.
 XX
 XX COLLISON EW, Hash SM, Choi I;
 XX
 XX MPI, 2002-315045/35.
 XX
 XX N-PDB; ABK48230.
 XX
 XX Polynucleotide encoding polypeptide of CD80 ligand, CD86 ligand, CD28
 PT receptor or CTLA-4 receptor as vaccine for inducing immune response in
 PT feline suffering from autoimmune disease or tissue or organ transplant.
 XX
 PS Disclosure; Fig 3a; 73pp; English.
 XX
 XX This invention relates to the DNA and protein sequences encoding a
 CC soluble CD80 ligand, soluble CD86 ligand, soluble and membrane-bound CD28
 CC receptor and soluble or membrane bound CTLA-4 receptor. The invention
 CC also relates to a vaccine comprising an effective amount of these
 CC receptor proteins. A vaccine is useful for inducing immunity or enhancing
 CC an immune response in a cat. The protein sequences of the invention are
 CC useful for suppressing an immune response in a feline suffering from an
 CC autoimmune disease or the recipient of a tissue or organ transplant. A
 CC vector containing the DNA sequences of the invention is useful for
 CC redirecting an immune response in a feline to an immunogen such as rabies
 CC virus, chlamydia, toxoplasmosis gondii, flea, feline immunodeficiency
 CC virus, feline leukemia (FeLV), feline infectious peritonitis virus
 CC (FIP), panleukopenia virus, calicivirus, reovirus type 3, rotavirus,
 CC coronavirus, syncytial virus, herpes virus, sarcoma virus, borna disease
 CC virus or a parasite. The protein sequences may be further utilised to
 CC promote growth in homologous or heterologous feline species. Enhancement
 CC of immunity through the interaction of soluble CD80 or soluble CD86 with
 CC CD28 or CTLA-4 or inhibition of an immune response through the
 CC interaction of feline CD80 or CD86 with CTLA4 takes advantage of the
 CC natural process of regulation rather than adding foreign substances that
 CC could have multiple, even detrimental effects on overall or long term
 CC health. The present sequence represents feline CD86 protein of the
 CC invention.
 XX
 XX Sequence 329 AA:
 SQ
 Query Match 4.2%; Score 14; DB 5; Length 329;
 Best Local Similarity 100.0%; Pred. No. 0.00011;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 87 WTLRLHNVQIKDKG 100
 Db 94 WTLRLHNVQIKDKG 107
 RESULT 8
 AAY41079
 ID AAY41079 standard; protein; 332 AA.
 XX
 AC AAY41079;

XX
 DT 20-DEC-1999 (first entry)
 XX
 DE Feline B7-2 protein.
 XX
 XX B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
 KM allergic reaction; infectious disease; tumor development; feline;
 KM graft rejection; inflammation; arthritis; atopic dermatitis; ss.
 XX
 OS Felis catus.
 XX
 XX WO9947558-A2.
 XX
 XX 23-SEP-1999.
 XX
 XX 19-MAR-1999; 99WO-US006187.
 XX
 XX 19-MAR-1998; 98US-0078765P.
 XX 17-APR-1998; 98US-00062597.
 XX
 XX (HESK-) HESKA CORP.
 XX
 XX Sim G, Yang S, Sellins KS;
 XX
 XX MPI, 1999-571822/48.
 XX
 XX N-PDB; AA227929; AA227931.
 XX
 XX New isolated B7 and CTLA4 nucleic acids, used to develop products for
 PT treating, e.g. autoimmune and atopic diseases.
 PT
 XX
 PS Claim 4; Page 116-119; 148pp; English.
 XX
 XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
 CC encoding nucleic acid molecules from dogs and cats. The proteins can be
 CC expressed by standard recombinant methodology. The nucleic acid molecules
 CC and the encoded proteins can be used for preventing or treating diseases,
 CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
 CC development, graft rejection, inflammation, arthritic and atopic diseases
 CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
 CC cats, cattle, sheep or pets. The products can also be used for detection,
 CC diagnosis and drug screening
 XX
 XX Sequence 332 AA:
 SQ
 Query Match 4.2%; Score 14; DB 2; Length 332;
 Best Local Similarity 100.0%; Pred. No. 0.00011;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 87 WTLRLHNVQIKDKG 100
 Db 94 WTLRLHNVQIKDKG 107
 RESULT 9
 AAY95333
 ID AAY95333 standard; peptide; 30 AA.
 XX
 AC AAY95333;
 XX
 XX 12-SEP-2003 (revised)
 DT 25-SEP-2000 (first entry)
 XX
 XX OVA323-339-p1g costimulatory molecule B7-2 epitope hybrid peptide 10.
 DE
 XX Co-stimulatory molecule; CD86; B7-2; p1g; immunosuppressive;
 KM xerograft transplantation; organ transplant; vaccine; B-cell epitope;
 KM T-cell epitope; ovalbumin; chicken.
 XX
 XX Gallus sp.
 OS
 OS Sus scrofa.
 OS
 XX Chimeric.
 XX
 FH Key Location/Qualifiers

```

FT Peptide 1..17
FT /note= "OVA323-339"
FT 18..30
FT Peptide /note= "B7-2 amino acids 76-88"
XX
XX WO200037102-A2.
XX
XX PD 29-JUN-2000.
XX
XX PF 17-DEC-1999; 99WO-GB004200.
XX
XX PR 19-DEC-1998; 98GB-00027921.
XX 23-OCT-1999; 99GB-00025015.
XX
XX (MLML-) ML LAB PLC.
XX
XX PI Lechler RI, Rogers NJ, Dorling A;
XX WPI; 2000-442537/38.
XX
XX PT Novel methods for improving tolerance to a xenograft comprising
XX immunizing a mammal with a T-cell epitope and a B-cell epitope.
XX
XX PS Disclosure; Page 23; 81pp; English.
XX
XX CC The present sequence is that of chimeric peptide 10 comprising T-cell
XX epitope OVA323-339 from chicken egg albumin (ovalbumin) and a B-cell
XX epitope comprising amino acids 76-88 of pig co-stimulatory molecule CD86
XX (B7-2) (see AAY95321). The invention relates to a novel strategy for
XX inhibiting costimulation by porcine cells of human T cells, with
XX particular importance in the context of xenotransplantation of porcine
XX organs. Recipients are immunised with hybrid synthetic peptides, such as
XX of the present peptide, comprising a T cell epitope conjugated to sequences
XX of the porcine costimulatory molecules CD80, CD86 or CD40. Peptides that
XX induce antibodies specific for regions of costimulatory molecules
XX involved in binding to their counter-receptors on human cells are capable
XX of blocking the delivery of costimulation. Once the antibody response has
XX been induced, the transplanted organ will recall this response due to the
XX expression of the costimulatory molecules, thereby sustaining the
XX response, and providing an endogenous mechanism of costimulatory
XX blockade. The method is useful for improving the tolerance of a host to
XX xenografts, particularly porcine pancreatic islet cells. (Updated on 12-
XX SEP-2003 to standardise OS field)
XX
XX SQ Sequence 30 AA;
XX
XX Query Match 3.9%; Score 13; DB 3; Length 30;
XX Best Local Similarity 100.0%; Pred. No. 0.00011;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 76 YMGRTSPDQATWT 88
XX |||||
XX 18 YMGRTSPDQATWT 30
XX
XX Db
XX
XX RESULT 10
XX AAY95327
XX ID AAY95327 standard; peptide; 30 AA.
XX
XX AC AAY95327;
XX
XX DT 12-SEP-2003 (revised)
XX 25-SEP-2000 (first entry)
XX
XX DE OVA323-339-pig costimulatory molecule B7-2 epitope hybrid peptide 3.
XX
XX KW Co-stimulatory molecule; CD86; B7-2; pig; immunosuppressive;
XX xenotransplantation; organ transplant; vaccine; B-cell epitope;
XX T-cell epitope; ovalbumin; chicken.
XX
XX OS Gallus sp.
XX OS Sus scrofa.
XX OS Chimeric.

```

```

XX
XX Key Location/Qualifiers
XX Peptide 1..17
XX /note= "OVA323-339"
XX 18..30
XX Peptide /note= "B7-2 amino acids 109-121"
XX
XX WO200037102-A2.
XX
XX PD 29-JUN-2000.
XX
XX PF 17-DEC-1999; 99WO-GB004200.
XX
XX PR 19-DEC-1998; 98GB-00027921.
XX 23-OCT-1999; 99GB-00025015.
XX
XX (MLML-) ML LAB PLC.
XX
XX PI Lechler RI, Rogers NJ, Dorling A;
XX WPI; 2000-442537/38.
XX
XX PT Novel methods for improving tolerance to a xenograft comprising
XX immunizing a mammal with a T-cell epitope and a B-cell epitope.
XX
XX PS Disclosure; Page 23; 81pp; English.
XX
XX CC The present sequence is that of chimeric peptide 3 comprising T-cell
XX epitope OVA323-339 from chicken egg albumin (ovalbumin) and a B-cell
XX epitope comprising amino acids 109-121 of pig co-stimulatory molecule
XX CD86 (B7-2) (see AAY95321). The invention relates to a novel strategy for
XX inhibiting costimulation by porcine cells of human T cells, with
XX particular importance in the context of xenotransplantation of porcine
XX organs. Recipients are immunised with hybrid synthetic peptides, such as
XX of the present peptide, comprising a T cell epitope conjugated to sequences
XX of the porcine costimulatory molecules CD80, CD86 or CD40. Peptides that
XX induce antibodies specific for regions of costimulatory molecules
XX involved in binding to their counter-receptors on human cells are capable
XX of blocking the delivery of costimulation. Once the antibody response has
XX been induced, the transplanted organ will recall this response due to the
XX expression of the costimulatory molecules, thereby sustaining the
XX response, and providing an endogenous mechanism of costimulatory
XX blockade. The method is useful for improving the tolerance of a host to
XX xenografts, particularly porcine pancreatic islet cells. (Updated on 12-
XX SEP-2003 to standardise OS field)
XX
XX SQ Sequence 30 AA;
XX
XX Query Match 3.9%; Score 13; DB 3; Length 30;
XX Best Local Similarity 100.0%; Pred. No. 0.00011;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 109 KGPFGLVPIHOMS 121
XX |||||
XX 18 KGPFGLVPIHOMS 30
XX
XX Db
XX
XX RESULT 11
XX AAY41080
XX ID AAY41080 standard; protein; 169 AA.
XX
XX AC AAY41080;
XX
XX DT 20-DEC-1999 (first entry)
XX
XX DE Feline B7-2 protein (larger fragment).
XX
XX KW B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
XX allergic reaction; infectious disease; tumor development; feline;
XX graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
XX OS Felis catus.
XX

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PN WO9947558-A2.
XX
XX 23-SEP-1999.
XX
XX 19-MAR-1999; 99WO-US006187.
XX
XX 19-MAR-1998; 98US-0078765P.
XX 17-APR-1998; 98US-00062597.
XX
XX (HESK-) HESKA CORP.
XX
XX Sim G, Yang S, Sellins KS;
XX WPI; 1999-571822/48.
XX N-PSDB; AA27933.
XX
XX New isolated B7 and CTLA4 nucleic acids, used to develop products for
XX treating, e.g. autoimmune and atopic diseases.
XX
XX Claim 4; Page 125-126; 148pp; English.
XX
XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
XX encoding nucleic acid molecules from dogs and cats. The proteins can be
XX expressed by standard recombinant methodology. The nucleic acid molecules
XX and the encoded proteins can be used for preventing or treating diseases,
XX e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
XX development, graft rejection, inflammation, arthritic and atopic diseases
XX such as atopic dermatitis. They can be used in mammals such humans, dogs,
XX cats, cattle, sheep or pets. The products can also be used for detection,
XX diagnosis and drug screening
XX
XX Sequence 169 AA:
XX
XX Query Match 3.9%; Score 13; DB 2; Length 169;
XX Best Local Similarity 100.0%; Pred. No. 0.00056;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 264 TLRRKKKQPPS 276
XX |||||
XX 110 TLRRKKKQPPS 122
XX
XX RESULT 12
XX ID AAY41078
XX AAY41078 standard; protein; 280 AA.
XX
XX AAY41078;
XX
XX 20-DEC-1999 (first entry)
XX
XX Canine B7-2s protein.
XX
XX B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
XX allergic reaction; infectious disease; tumor development; canine;
XX graft rejection; inflammation; arthritis; atopic dermatitis.
XX
XX Canis familiaris.
XX
XX WO9947558-A2.
XX
XX 23-SEP-1999.
XX
XX 19-MAR-1999; 99WO-US006187.
XX
XX 19-MAR-1998; 98US-0078765P.
XX 17-APR-1998; 98US-00062597.
XX
XX (HESK-) HESKA CORP.
XX
XX Sim G, Yang S, Sellins KS;
XX WPI; 1999-571822/48.
XX N-PSDB; AA27921, AA27923.

```

```

XX
XX New isolated B7 and CTLA4 nucleic acids, used to develop products for
XX treating, e.g. autoimmune and atopic diseases.
XX
XX Claim 4; Page 109-111; 148pp; English.
XX
XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
XX encoding nucleic acid molecules from dogs and cats. The proteins can be
XX expressed by standard recombinant methodology. The nucleic acid molecules
XX and the encoded proteins can be used for preventing or treating diseases,
XX e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
XX development, graft rejection, inflammation, arthritic and atopic diseases
XX such as atopic dermatitis. They can be used in mammals such humans, dogs,
XX cats, cattle, sheep or pets. The products can also be used for detection,
XX diagnosis and drug screening
XX
XX Sequence 280 AA:
XX
XX Query Match 3.9%; Score 13; DB 2; Length 280;
XX Best Local Similarity 100.0%; Pred. No. 0.0009;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 29 TGEUPCHFTNSON 41
XX |||||
XX 35 TGEUPCHFTNSON 47
XX
XX RESULT 13
XX ID AAY41076
XX AAY41076 standard; protein; 329 AA.
XX
XX AAY41076;
XX
XX 20-DEC-1999 (first entry)
XX
XX Canine B7-2 protein.
XX
XX B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
XX allergic reaction; infectious disease; tumor development; canine;
XX graft rejection; inflammation; arthritis; atopic dermatitis.
XX
XX Canis familiaris.
XX
XX WO9947558-A2.
XX
XX 23-SEP-1999.
XX
XX 19-MAR-1999; 99WO-US006187.
XX
XX 19-MAR-1998; 98US-0078765P.
XX 17-APR-1998; 98US-00062597.
XX
XX (HESK-) HESKA CORP.
XX
XX Sim G, Yang S, Sellins KS;
XX WPI; 1999-571822/48.
XX N-PSDB; AA27913, AA27915.
XX
XX New isolated B7 and CTLA4 nucleic acids, used to develop products for
XX treating, e.g. autoimmune and atopic diseases.
XX
XX Claim 4; Page 97-99; 148pp; English.
XX
XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
XX encoding nucleic acid molecules from dogs and cats. The proteins can be
XX expressed by standard recombinant methodology. The nucleic acid molecules
XX and the encoded proteins can be used for preventing or treating diseases,
XX e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
XX development, graft rejection, inflammation, arthritic and atopic diseases
XX such as atopic dermatitis. They can be used in mammals such humans, dogs,
XX cats, cattle, sheep or pets. The products can also be used for detection,
XX diagnosis and drug screening

```


CC response, and providing an endogenous mechanism of costimulatory
 CC blockade. The method is useful for improving the tolerance of a host to
 CC xenografts, particularly porcine pancreatic islet cells. (Updated on 12-
 CC SEP-2003 to standardise OS field)
 XX

SQ Sequence 29 AA;

Query Match 3.6%; Score 12; DB 3; Length 29;
 Best Local Similarity 100.0%; Pred. No. 0.001;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 ASLKSQAYFNET 29
 |||||
 Db 18 ASLKSQAYFNET 29

Search completed: December 15, 2004, 16:56:55
 Job time : 158 secs

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OM protein - protein search, using sw model

Run on: December 15, 2004, 16:50:43 ; Search time 39 Seconds

(without alignments)
561.152 Million cell updates/sec

Title: US-09-868-605-14

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Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	325	98.5	325	4 US-09-651-200-20	Sequence 20, Appl
2	14	4.2	328	4 US-09-651-200-18	Sequence 18, Appl
3	14	4.2	328	4 US-09-303-040-6	Sequence 6, Appl
4	13	3.9	329	4 US-09-651-200-19	Sequence 19, Appl
5	12	3.6	95	3 US-08-928-3838-10	Sequence 10, Appl
6	12	3.6	303	4 US-09-651-200-23	Sequence 23, Appl
7	12	3.6	303	4 US-09-441-411-15	Sequence 15, Appl
8	12	3.6	303	4 US-09-441-411-20	Sequence 20, Appl
9	12	3.6	308	2 US-08-456-104-4	Sequence 2, Appl
10	12	3.6	309	3 US-08-479-744A-23	Sequence 23, Appl
11	12	3.6	309	3 US-08-280-757B-23	Sequence 23, Appl
12	12	3.6	309	3 US-08-205-697A-21	Sequence 21, Appl
13	12	3.6	309	3 US-08-702-525-21	Sequence 21, Appl
14	12	3.6	309	3 US-09-651-200-22	Sequence 22, Appl
15	12	3.6	309	4 US-09-667-135-33	Sequence 33, Appl
16	12	3.6	309	4 US-09-425-762-23	Sequence 23, Appl
17	12	3.6	309	4 US-09-837-867A-21	Sequence 21, Appl
18	12	3.6	309	4 US-09-206-132-4	Sequence 4, Appl
19	12	3.6	309	4 US-09-441-411-13	Sequence 13, Appl
20	12	3.6	309	4 US-09-441-411-18	Sequence 18, Appl
21	12	3.6	309	5 PCT-US95-02576-21	Sequence 21, Appl
22	12	3.6	309	5 PCT-US94-09642-2	Sequence 2, Appl
23	12	3.6	314	3 US-08-205-697A-13	Sequence 13, Appl
24	12	3.6	314	3 US-08-702-525-13	Sequence 13, Appl
25	12	3.6	314	4 US-09-837-867A-13	Sequence 13, Appl
26	12	3.6	314	4 US-09-441-411-14	Sequence 14, Appl
27	12	3.6	314	4 US-09-441-411-19	Sequence 19, Appl

28	12	3.6	314	5 PCT-US95-02576-13	Sequence 13, Appl
29	12	3.6	339	4 US-09-719-243-2	Sequence 2, Appl
30	12	3.6	356	4 US-09-441-411-11	Sequence 11, Appl
31	12	3.6	356	4 US-09-441-411-12	Sequence 12, Appl
32	12	3.6	356	4 US-09-441-411-16	Sequence 16, Appl
33	12	3.6	356	4 US-09-441-411-17	Sequence 17, Appl
34	12	3.6	358	4 US-09-719-243-3	Sequence 3, Appl
35	10	3.0	16	3 US-08-205-697A-42	Sequence 42, Appl
36	10	3.0	16	3 US-08-702-525-42	Sequence 42, Appl
37	10	3.0	16	4 US-09-837-867A-42	Sequence 42, Appl
38	10	3.0	16	5 PCT-US95-02576-42	Sequence 42, Appl
39	10	3.0	102	4 US-09-513-999C-4502	Sequence 4502, Ap
40	10	3.0	110	3 US-08-479-744A-45	Sequence 45, Appl
41	10	3.0	110	3 US-08-280-757B-45	Sequence 45, Appl
42	10	3.0	110	4 US-09-425-762-45	Sequence 45, Appl
43	10	3.0	323	4 US-09-651-200-21	Sequence 21, Appl
44	10	3.0	323	4 US-09-441-411-22	Sequence 22, Appl
45	10	3.0	323	5 PCT-US94-09642-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-651-200-20
Sequence 20, Application US/09651200
Patent No. 6429303
GENERAL INFORMATION:
APPLICANT: Green et al
TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B
TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and
FILE REFERENCE: 15966-563 (CUTR-62)
CURRENT APPLICATION NUMBER: US/09/651,200
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/152383
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/172909
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/183578
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 20
LENGTH: 325
TYPE: PRT
ORGANISM: sus sp.
US-09-651-200-20

Query Match 98.5%; Score 325; DB 4; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.3e-117;
Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGLSNILFVWVLLSGAASLKSQAYFNETGELPHFTNSQSLDELYIFWQDDNLYL	60
DB	1	MGLSNILFVWVLLSGAASLKSQAYFNETGELPHFTNSQSLDELYIFWQDDNLYL	60
QY	61	ELYRQEXPHNVNKSVMGRTSFDQATWTLRLAHVQIDKDSYQCFIHKKGHGLVPIHOM	120
DB	61	ELYRQEXPHNVNKSVMGRTSFDQATWTLRLAHVQIDKDSYQCFIHKKGHGLVPIHOM	120
QY	121	SSDSLILNFQPEINILTNHTENSVINLTSSIQGYPBPQRMMLNTKSTTEHDADY	180
DB	121	SSDSLILNFQPEINILTNHTENSVINLTSSIQGYPBPQRMMLNTKSTTEHDADY	180
QY	181	KKSQNNITELNVSRVSLPIPETNNSIVCVLQLESKTLFSLPCNIDAKPPVQFPVP	240
DB	181	KKSQNNITELNVSRVSLPIPETNNSIVCVLQLESKTLFSLPCNIDAKPPVQFPVP	240
QY	241	DHILMIALVTVVVVGCMVSFTLRLRRKKQPPSPNECGTTIKNRKASQTKRRAEVH	300
DB	241	DHILMIALVTVVVVGCMVSFTLRLRRKKQPPSPNECGTTIKNRKASQTKRRAEVH	300

QY 301 ERSDDACDVNIIKTASDNDSTDF 325
| | | | |
Db 301 ERSDDACDVNIIKTASDNDSTDF 325

RESULT 2
US-09-651-200-18
; Sequence 18, Application US/09651200
; Patent No. 6429303
; GENERAL INFORMATION:
; APPLICANT: Green et al
; TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B
; TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 15966-562 (CURA-62)
; CURRENT APPLICATION NUMBER: US/09/651,200
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/152383
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/172909
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/183578
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 18
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Felis catus
US-09-651-200-18

Query Match 4.2%; Score 14; DB 4; Length 329;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 WTLRLHNVQIKDKG 100
| | | | |
Db 94 WTLRLHNVQIKDKG 107

RESULT 3
US-09-303-040-6
; Sequence 6, Application US/09303040
; Patent No. 6555671
; GENERAL INFORMATION:
; APPLICANT: Winslow, Barbara J.
; APPLICANT: Cochran, Mark D.
; TITLE OF INVENTION: Recombinant Virus Expressing Foreign DNA Encoding
; TITLE OF INVENTION: Feline CD80, Feline CD86, Feline CTLA-4 or
; TITLE OF INVENTION: Feline Interferon-gamma And Uses Thereof
; FILE REFERENCE: 54957-B
; CURRENT APPLICATION NUMBER: US/09/303,040
; CURRENT FILING DATE: 1999-04-30
; EARLIER APPLICATION NUMBER: 60/083,870
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 329
; TYPE: PRT
; ORGANISM: feline CD86
US-09-303-040-6

Query Match 4.2%; Score 14; DB 4; Length 329;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 WTLRLHNVQIKDKG 100
| | | | |
Db 94 WTLRLHNVQIKDKG 107

RESULT 4

US-09-651-200-19
; Sequence 19, Application US/09651200
; Patent No. 6429303
; GENERAL INFORMATION:
; APPLICANT: Green et al
; TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B
; TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 15966-562 (CURA-62)
; CURRENT APPLICATION NUMBER: US/09/651,200
; CURRENT FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/152383
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/172909
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/183578
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 19
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-651-200-19

Query Match 3.9%; Score 13; DB 4; Length 329;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 TGEIPLCHFTNSON 41
| | | | |
Db 35 TGEIPLCHFTNSON 47

RESULT 5
US-08-928-383B-10
; Sequence 10, Application US/08928383B
; Patent No. 6210921
; GENERAL INFORMATION:
; APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,
; APPLICANT: and Marshall S. Horvitz,
; TITLE OF INVENTION: CAR, A No. 6210921e1 Coxsackievirus and Adenovirus
; TITLE OF INVENTION: Receptor
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,383B
; FILING DATE: 12-SEP-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,100
; FILING DATE: 13-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: DFN-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 95 amino acids

Thu Dec 16 12:21:13 2004

us-09-868-605-14.Oligo.rat

Page 3

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-928-383B-10

Query Match 3.6%; Score 12; DB 3; Length 95;
Best Local Similarity 100.0%; Pred. No. 0.00035;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 WTLRLHNVQIKD 98
Db 61 WTLRLHNVQIKD 72

RESULT 6
US-09-651-200-23
Sequence 23, Application US/09651200
Patent No. 6429303
GENERAL INFORMATION:
APPLICANT: Green et al
TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B
TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 15966-562 (CURA-62)
CURRENT APPLICATION NUMBER: US/09/651,200
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/152383
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/172909
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/183578
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 23
LENGTH: 303
TYPE: PRT
ORGANISM: Mus musculus
US-09-651-200-23

Query Match 3.6%; Score 12; DB 4; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 WTLRLHNVQIKD 98
Db 87 WTLRLHNVQIKD 98

RESULT 7
US-09-441-411-15
Sequence 15, Application US/09441411
Patent No. 6734172
GENERAL INFORMATION:
APPLICANT: Scholler, Nathalie B.
APPLICANT: Disis, Mary L.
APPLICANT: Hellstrom, Ingegerd
APPLICANT: Hellstrom, Karl Erik
TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
FILE REFERENCE: 730033.409
CURRENT APPLICATION NUMBER: US/09/441,411
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15
LENGTH: 303
TYPE: PRT
ORGANISM: Mus musculus
US-09-441-411-15
Query Match 3.6%; Score 12; DB 4; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.001;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 WTLRLHNVQIKD 98
Db 87 WTLRLHNVQIKD 98

RESULT 8
US-09-441-411-20
Sequence 20, Application US/09441411
Patent No. 6734172
GENERAL INFORMATION:
APPLICANT: Scholler, Nathalie B.
APPLICANT: Disis, Mary L.
APPLICANT: Hellstrom, Ingegerd
APPLICANT: Hellstrom, Karl Erik
TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
FILE REFERENCE: 730033.409
CURRENT APPLICATION NUMBER: US/09/441,411
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20
LENGTH: 303
TYPE: PRT
ORGANISM: Mus musculus
US-09-441-411-20

Query Match 3.6%; Score 12; DB 4; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 WTLRLHNVQIKD 98
Db 87 WTLRLHNVQIKD 98

RESULT 9
US-08-456-104-4
Sequence 4, Application US/08456104
Patent No. 5861310
GENERAL INFORMATION:
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASED
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,104
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/101,624;
FILING DATE: 26-JUL-1993;
APPLICATION NUMBER: 08/109,393;
APPLICATION NUMBER: 19-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPT-008
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-456-104-4

Query Match 3.6%; Score 12; DB 2; Length 309;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 WTLRLHNVQIKD 98
Db 93 WTLRLHNVQIKD 104

RESULT 10

US-08-479-744A-23
Sequence 23, Application US/08479744A
Patent No. 6084067
GENERAL INFORMATION:
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: No. 6084067e1 CTLA4/CD28 Ligands and
TITLE OF INVENTION: Uses Therefor
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,744A
FILING DATE: June 7, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/280,757
FILING DATE: 26-JUL-1994
APPLICATION NUMBER: 08/109,393
FILING DATE: 28-AUG-1993
APPLICATION NUMBER: 08/101,624
FILING DATE: 26-JULY-1993
APPLICATION NUMBER: 08/147,773
FILING DATE: 3-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-004CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-479-744A-23

Query Match 3.6%; Score 12; DB 3; Length 309;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 WTLRLHNVQIKD 98
Db 93 WTLRLHNVQIKD 104

RESULT 11

US-08-280-757B-23
Sequence 23, Application US/08280757B
Patent No. 6130316
GENERAL INFORMATION:
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: No. 6130316e1 CTLA4/CD28 Ligands and
TITLE OF INVENTION: Uses Therefor
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/280,757B
FILING DATE: 26-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/101,624
FILING DATE: 26-JULY-1993
APPLICATION NUMBER: 08/109,393
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: 08/147,773
FILING DATE: 3-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-004CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-280-757B-23

Query Match 3.6%; Score 12; DB 3; Length 309;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 WTLRLHNVQIKD 98
Db 93 WTLRLHNVQIKD 104

RESULT 12

US-08-205-697A-21
Sequence 21, Application US/08205697A
Patent No. 6218510
GENERAL INFORMATION:
APPLICANT: Sharpe, Arlene H.
APPLICANT: Borriello, Francescopaulo
APPLICANT: Freeman, Gordon J.

```
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: No. 6218510e1 Forms of T Cell Costimulatory Molecules
TITLE OF INVENTION: and Uses therefor
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/205,697A
FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: BHI-120
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-205-697A-21

Query Match          3.6%; Score 12; DB 3; Length 309;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      87 WTLRLHNVQIKD 98
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Db      93 WTLRLHNVQIKD 104

RESULT 13
US-08-702-525-21
Sequence 21, Application US/08702525
Patent No. 6294660
GENERAL INFORMATION:
APPLICANT: Sharpe, Sharpe
APPLICANT: Freeman, Gordon
APPLICANT: Nadler, Lee
TITLE OF INVENTION: No. 6294660e1 Forms of T Cell Costimulatory
Molecules and Uses therefor
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,525
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/205,697
FILING DATE: 02-Mar-1994
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ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: BHI-120CPUS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-702-525-21

Query Match          3.6%; Score 12; DB 3; Length 309;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      87 WTLRLHNVQIKD 98
      |||||||
Db      93 WTLRLHNVQIKD 104

RESULT 14
US-09-651-200-22
Sequence 22, Application US/09651200
Patent No. 6429303
GENERAL INFORMATION:
APPLICANT: Green et al
TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B
Lymphocyte Activation Antigen B-7 Family and
FILE REFERENCE: 15966-562 (CRA-62)
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: US/09/651,200
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/152363
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/183578
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentia Ver. 2.0
SEQ ID NO 22
LENGTH: 309
TYPE: PRT
ORGANISM: Mus musculus
US-09-651-200-22

Query Match          3.6%; Score 12; DB 4; Length 309;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      87 WTLRLHNVQIKD 98
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Db      93 WTLRLHNVQIKD 104

RESULT 15
US-09-667-135-33
Sequence 33, Application US/09667135
Patent No. 6521749
GENERAL INFORMATION:
APPLICANT: Vincent Ling
APPLICANT: Kyriaki Damsel-Joannopoulos
TITLE OF INVENTION: NOVEL GL50 MOLECULES AND USES THEREFOR
FILE REFERENCE: GNN-007
CURRENT APPLICATION NUMBER: US/09/667,135
CURRENT FILING DATE: 2000-09-21
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 33
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LENGTH: 309
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
OTHER INFORMATION:
US-09-667-135-33

Query Match 3.6%; Score 12; DB 4; Length 309;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 87 WTLRLHNVQIKD 98
|||
Db 93 WTLRLHNVQIKD 104

Search completed: December 15, 2004, 17:01:49
Job time : 41 secs

Thu Dec 16 12:21:13 2004

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Page 1

Gencore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 15, 2004, 17:00:25 ; Search time 144 Seconds

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Title: US-09-868-605-14

Perfect score: 330

Sequence: 1 MGLSNILFWVLLSGASL.....NLTAKSDNDSTYDLKSL 330

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Word size : 0

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Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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16: /cg2_6/prodata/2/pubppa/US10D_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	14	4.2	332	16	US-10-790-396-26
4	13	3.9	169	16	US-10-790-396-31
5	13	3.9	280	16	US-10-790-396-17
6	13	3.9	329	16	US-10-790-396-7
7	12	3.6	323	13	US-10-087-192-1077
8	12	3.6	303	10	US-09-441-411-15
9	12	3.6	303	10	US-09-441-411-20
10	12	3.6	303	17	US-10-762-128-15
11	12	3.6	303	17	US-10-762-128-20
12	12	3.6	309	9	US-09-425-762-23
13	12	3.6	309	9	US-09-837-867A-21

14	12	3.6	309	10	US-09-441-411-13	Sequence 13, Appl
15	12	3.6	309	10	US-09-441-411-18	Sequence 18, Appl
16	12	3.6	309	10	US-09-441-411-24	Sequence 24, Appl
17	12	3.6	309	10	US-09-441-411-19	Sequence 19, Appl
18	12	3.6	309	15	US-10-318-855-33	Sequence 33, Appl
19	12	3.6	309	17	US-10-643-768-21	Sequence 21, Appl
20	12	3.6	309	17	US-10-762-128-13	Sequence 13, Appl
21	12	3.6	309	17	US-10-762-128-18	Sequence 18, Appl
22	12	3.6	309	17	US-10-762-128-24	Sequence 24, Appl
23	12	3.6	309	17	US-10-429-079B-23	Sequence 23, Appl
24	12	3.6	314	9	US-09-837-867A-13	Sequence 13, Appl
25	12	3.6	314	10	US-09-441-411-13	Sequence 14, Appl
26	12	3.6	314	10	US-09-441-411-19	Sequence 19, Appl
27	12	3.6	314	10	US-09-441-411-15	Sequence 15, Appl
28	12	3.6	314	17	US-10-643-768-13	Sequence 13, Appl
29	12	3.6	314	17	US-10-643-768-14	Sequence 14, Appl
30	12	3.6	314	17	US-10-762-128-14	Sequence 14, Appl
31	12	3.6	339	15	US-10-727-000-2	Sequence 2, Appl
32	12	3.6	356	10	US-09-441-411-11	Sequence 11, Appl
33	12	3.6	356	10	US-09-441-411-12	Sequence 12, Appl
34	12	3.6	356	10	US-09-441-411-16	Sequence 16, Appl
35	12	3.6	356	10	US-09-441-411-17	Sequence 17, Appl
36	12	3.6	356	17	US-10-762-128-11	Sequence 11, Appl
37	12	3.6	356	17	US-10-762-128-12	Sequence 12, Appl
38	12	3.6	356	17	US-10-762-128-16	Sequence 16, Appl
39	12	3.6	356	17	US-10-762-128-17	Sequence 17, Appl
40	12	3.6	358	15	US-10-727-000-3	Sequence 3, Appl
41	10	3.0	16	9	US-09-837-867A-42	Sequence 42, Appl
42	10	3.0	16	10	US-09-962-969-42	Sequence 42, Appl
43	10	3.0	16	17	US-10-643-768-42	Sequence 42, Appl
44	10	3.0	104	16	US-10-696-259-18	Sequence 16, Appl
45	10	3.0	110	9	US-09-425-762-45	Sequence 45, Appl

ALIGNMENTS

RESULT 1
US-09-303-510-6
; Sequence 6, Application US/09303510A
; Patent No. US20020028208A1
; GENERAL INFORMATION:
; APPLICANT: Collisson, Ellen W.
; APPLICANT: Hash, Stephen M.
; TITLE OF INVENTION: Feline CD80, Feline CD86, Feline CD28, and Feline
; FILE REFERENCE: 54954
; CURRENT APPLICATION NUMBER: US/09/303,510A
; CURRENT FILING DATE: 1999-04-30
; EARLIER APPLICATION NUMBER: 60/083,869
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Feline
US-09-303-510-6
Query Match 4.2%; Score 14; DB 9; Length 329;
Best Local Similarity 100.0%; Pred. No. 8.1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 87 WTIRLHNQIDKRG 100
DB 94 WTIRLHNQIDKRG 107
RESULT 2
US-09-303-040-6
; Sequence 6, Application US/09303040
; Patent No. US20020051792A1

RESULT 6
 US-10-790-396-7
 ; Sequence 7, Application US/10790396
 ; Publication No. US20040157296A1
 ; GENERAL INFORMATION: "
 ; APPLICANT: Sim, Gek-Xee
 ; APPLICANT: Yang, Shumin
 ; APPLICANT: Sellins, Karen S.
 ; TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY
 ; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
 ; PROTEINS, NUCLEIC

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```
FILE REFERENCE: IM-1-C1-PCT
CURRENT APPLICATION NUMBER: US/10/790,396
CURRENT FILING DATE: 2004-03-01
PRIOR APPLICATION NUMBER: US/09/646,561
PRIOR FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: 60/078,765
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 09/062,597
PRIOR FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 329
TYPE: PRT
ORGANISM: Canis familiaris
US-10-790-396-7
```

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Query Match      3.9%; Score 13; DB 16; Length 329;
Best Local Similarity 100.0%; Pred. No. 0.00076;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      29 TGEIPECHTNSQN 41
DB      35 TGEIPECHTNSQN 47
```

```
RESULT 7
US-10-087-192-1077
Sequence 1077, Application US/10087192
Publication No. US20020182586A1
GENERAL INFORMATION:
APPLICANT: Morris, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
FILE REFERENCE: 52945200122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1077
LENGTH: 230
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1) -- (230)
OTHER INFORMATION: Xaa = Any Amino Acid
US-10-087-192-1077
```

```
Query Match      3.6%; Score 12; DB 13; Length 230;
Best Local Similarity 100.0%; Pred. No. 0.0052;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      87 WTLRLHNVQIKD 98
DB      90 WTLRLHNVQIKD 101
```

```
RESULT 8
US-09-441-411-15
Sequence 15, Application US/09441411
Publication No. US20030008342A1
GENERAL INFORMATION:
APPLICANT: Scholler, Nathalie B.
APPLICANT: Disis, Mary L.
APPLICANT: Hellstrom, Ingegerd
APPLICANT: Hellstrom, Karl Erik
TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
```

```
FILE REFERENCE: 730033.409
CURRENT APPLICATION NUMBER: US/09/441,411
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15
LENGTH: 303
TYPE: PRT
ORGANISM: Mus musculus
US-09-441-411-15
```

```
Query Match      3.6%; Score 12; DB 10; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.0067;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      87 WTLRLHNVQIKD 98
DB      87 WTLRLHNVQIKD 98
```

```
RESULT 9
US-09-441-411-20
Sequence 20, Application US/09441411
Publication No. US20030008342A1
GENERAL INFORMATION:
APPLICANT: Scholler, Nathalie B.
APPLICANT: Disis, Mary L.
APPLICANT: Hellstrom, Ingegerd
APPLICANT: Hellstrom, Karl Erik
TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
FILE REFERENCE: 730033.409
CURRENT APPLICATION NUMBER: US/09/441,411
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20
LENGTH: 303
TYPE: PRT
ORGANISM: Mus musculus
US-09-441-411-20
```

```
Query Match      3.6%; Score 12; DB 10; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.0067;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      87 WTLRLHNVQIKD 98
DB      87 WTLRLHNVQIKD 98
```

```
RESULT 10
US-10-762-128-15
Sequence 15, Application US/10762128
Publication No. US20040219161A1
GENERAL INFORMATION:
APPLICANT: Scholler, Nathalie B.
APPLICANT: Disis, Mary L.
APPLICANT: Hellstrom, Ingegerd
APPLICANT: Hellstrom, Karl Erik
TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
FILE REFERENCE: 730033.409C1
CURRENT APPLICATION NUMBER: US/10/762,128
CURRENT FILING DATE: 2004-01-20
PRIOR APPLICATION NUMBER: US 09/441,411
PRIOR FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15
LENGTH: 303
TYPE: PRT
ORGANISM: Mus musculus
US-10-762-128-15
```

Query Match 3.6%; Score 12; DB 17; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.0067;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 WTLRHNVQIKD 98
DB 87 WTLRHNVQIKD 98

RESULT 11
US-10-762-128-20
; Sequence 20, Application US/10762128
; Publication No. US20040219161A1
; GENERAL INFORMATION:
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Disis, Mary L.
; APPLICANT: Helstrom, Ingegerd
; APPLICANT: Helstrom, Karl Erik
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 730033.409C1
; CURRENT APPLICATION NUMBER: US/10/762,128
; CURRENT FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 09/441,411
; PRIOR FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-762-128-20

Query Match 3.6%; Score 12; DB 17; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.0067;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 WTLRHNVQIKD 98
DB 87 WTLRHNVQIKD 98

RESULT 12
US-09-425-762-23
; Sequence 23, Application US/09425762
; Publication No. US20020086414A1
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: No. 6605279e1 CTLA4/CD28 ligands and
; TITLE OF INVENTION: Uses Therefor
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/425,762
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/479,744
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-004CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-425-762-23

Query Match 3.6%; Score 12; DB 9; Length 309;
Best Local Similarity 100.0%; Pred. No. 0.0068;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 WTLRHNVQIKD 98
DB 93 WTLRHNVQIKD 104

RESULT 13
US-09-837-867A-21
; Sequence 21, Application US/09837867A
; Patent No. US20020098542A1
; GENERAL INFORMATION:
; APPLICANT: Sharpe, Arlene H.
; APPLICANT: Bottiello, Francescopaulo
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; TITLE OF INVENTION: No. US20020098542A1e1 Forms of T Cell Costimulatory
; FILE REFERENCE: BWI-120CPADV
; CURRENT APPLICATION NUMBER: US/09/837,867A
; CURRENT FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 08/205,697
; PRIOR FILING DATE: 1994-03-02
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-837-867A-21

Query Match 3.6%; Score 12; DB 9; Length 309;
Best Local Similarity 100.0%; Pred. No. 0.0068;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 WTLRHNVQIKD 98
DB 93 WTLRHNVQIKD 104

RESULT 14
US-09-441-411-13
; Sequence 13, Application US/09441411
; Publication No. US20030008342A1
; GENERAL INFORMATION:
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Disis, Mary L.
; APPLICANT: Helstrom, Ingegerd
; APPLICANT: Helstrom, Karl Erik
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 730033.409
; CURRENT APPLICATION NUMBER: US/09/441,411
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 309
; TYPE: PRT

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Page 5

ORGANISM: Mus musculus
US-09-441-411-13

Query Match 3.6%; Score 12; DB 10; Length 309;
Best Local Similarity 100.0%; Pred. No. 0.0068;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 87 WTLRLHNVQIKD 98
|||||
Db 93 WTLRLHNVQIKD 104

RESULT 15
US-09-441-411-18
; Sequence 18; Application US/09441411
; Publication No. US20030008342A1
; GENERAL INFORMATION:
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Disis, Mary L.
; APPLICANT: Helstrom, Ingegerd
; APPLICANT: Helstrom, Karl Erik
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 73003.409
; CURRENT APPLICATION NUMBER: US/09/441,411
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-441-411-18

Query Match 3.6%; Score 12; DB 10; Length 309;
Best Local Similarity 100.0%; Pred. No. 0.0068;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 87 WTLRLHNVQIKD 98
|||||
Db 93 WTLRLHNVQIKD 104

Search completed: December 15, 2004, 17:12:44
Job time : 145 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 15, 2004, 16:50:10 ; Search time 40 Seconds
(without alignments)
793.788 Million cell updates/sec

Title: US-09-868-605-14

Perfect score: 330
Sequence: 1 MGLSNILFVMVLLSGAASL.....NLIKASDNDSTTDFLKSRL 330

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
1	12	3.6	109	2	gene B7-2 protein
2	10	3.0	110	2	CD86 spliced varia
3	10	3.0	275	2	CD86 spliced varia
4	10	3.0	329	1	B7-2 antigen - hum
5	10	3.0	330	2	CD86 precursor - r
6	8	2.4	298	2	hypothetical prote
7	8	2.4	354	2	YGP1 protein precu
8	8	2.4	823	2	probable membrane
9	8	2.4	823	2	HLA-A2 - human (fr
10	7	2.1	20	2	mannose-specific l
11	7	2.1	34	2	lectin - shalio
12	7	2.1	83	1	E7 protein - human
13	7	2.1	101	2	hypothetical prote
14	7	2.1	135	2	hypothetical prote
15	7	2.1	149	2	hypothetical prote
16	7	2.1	154	2	conserved hypothet
17	7	2.1	176	2	hypothetical prote
18	7	2.1	194	2	probable ribosomal
19	7	2.1	207	2	ribosomal protein
20	7	2.1	229	2	conserved hypothet
21	7	2.1	242	2	MADS box protein D
22	7	2.1	243	2	hypothetical prote
23	7	2.1	256	1	protease 3 (EC 3
24	7	2.1	256	2	hypothetical prote
25	7	2.1	261	2	hypothetical prote
26	7	2.1	266	2	hypothetical prote
27	7	2.1	317	2	ORF MSV16 hypothe
28	7	2.1	324	2	outer membrane pro
29	7	2.1	331	2	hypothetical prote

30	7	2.1	343	2	S44721	outer membrane pro
31	7	2.1	347	2	S15171	outer membrane pro
32	7	2.1	347	2	S15172	outer membrane pro
33	7	2.1	347	2	T35013	probable membrane
34	7	2.1	348	2	S15175	outer membrane pro
35	7	2.1	348	2	S15170	outer membrane pro
36	7	2.1	348	2	S44720	outer membrane pro
37	7	2.1	349	2	S15173	outer membrane pro
38	7	2.1	350	2	S44718	outer membrane pro
39	7	2.1	350	2	S15176	outer membrane pro
40	7	2.1	350	2	S44717	outer membrane pro
41	7	2.1	351	2	S20537	outer membrane pro
42	7	2.1	352	2	S15177	outer membrane pro
43	7	2.1	354	2	S44724	outer membrane pro
44	7	2.1	354	2	S22757	outer membrane pro
45	7	2.1	354	2	S44725	outer membrane pro

ALIGNMENTS

RESULT 1
149522
Gene B7-2 protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: 149522
R:Freeman, G.J.; Borriello, F.; Hodges, R.J.; Reiser, H.; Gribben, J.G.; Ng, J.W.; Kim, J.
J. Exp. Med. 178, 2185-2192, 1993
A>Title: Murine B7-2, an alternative CTLA4 counter-receptor that costimulates T cell pr
A:Reference number: 149522; MUID:94065585; PMID:7504059
A:Accession: 149522
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-309 <RES>
A:Cross-references: UNIPROT:P42082; GB:L25606; NID:G432478; PIDN:AAA79770.1; PID:G43247
C:Genetics:
A:Gene: B7-2
C:Superfamily: B7-2 antigen

Query Match 3.6%; Score 12; DB 2; Length 309;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 12; Conservative 0; Mismatches 0; Indels 0;

QY 87 WTLRLHNVQIKD 98
DB 93 WTLRLHNVQIKD 104

RESULT 2

UC7605
CD86 spliced variant CD86 deltaEC isoform - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C:Accession: UC7605
R:Magistrelli, G.; Caron, G.; Gauchat, J.F.; Jeanmou, P.; Bonnefoy, J.Y.; Delneste, Y.
Biochem. Biophys. Res. Commun. 280, 1211-1215, 2001
A>Title: Identification of an alternatively spliced variant of human CD86 mRNA.
A:Reference number: UC7604; MUID:21092744; PMID:11162656
A:Accession: UC7605
A:Molecule type: mRNA
A:Residues: 1-110 <MAG>
A:Cross-references: UNIPROT:P42081
C:Comment: This CD86 variant expressed by nonstimulated human monocytes, as a membrane
tion.
C:Genetics:
A:Gene: cd86deltaEC

Query Match 3.0%; Score 10; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSNILFVM 10

Db 1 MGLSNILFVM 10

RESULT 3
 CD86 spliced variant CD86 deltaTM isoform - human
 C/Species: Homo sapiens (man)
 C/Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 18-Nov-2002
 C/Accession: J07604
 R/Magistrelli, G.; Caron, G.; Gauchat, J.F.; Jeannin, P.; Bonnefoy, J.Y.; Delneste, Y.
 Biochem. Biophys. Res. Commun. 280, 1211-1215, 2001
 A/Title: Identification of an alternatively spliced variant of human CD86 mRNA.
 A/Reference number: J07604; MUID:21092744; PMID:11162656
 A/Accession: J07604
 A/Molecule type: mRNA
 A/Residues: 1-275 <MAG>
 C/Comment: This CD86 variant expressed by activated human monocytes, is a costimulatory
 C/Genetics:
 A/Gene: cd86deltaTM
 C/Superfamily: B-lymphocyte restricted antigen B7
 C/Keywords: immune response

Query Match 3.0%; Score 10; DB 2; Length 275;
 Best Local Similarity 100.0%; Pred. No. 0.042;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLSNILFVM 10

RESULT 4
 B7-2 antigen - human
 N/Alternate names: B70 glycoprotein; CD86 antigen; CTLA-4 counter-receptor
 C/Species: Homo sapiens (man)
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C/Accession: A48754; S39055
 R/Freeman, G.J.; Gridben, J.G.; Boussiotis, V.A.; NG, J.W.; Restivo Jr., V.A.; Lombard, S.
 Science 262, 909-911, 1993
 A/Title: Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human T cell proliferation.
 A/Reference number: A48754; MUID:94053735; PMID:7694363
 A/Accession: A48754
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-329 <FRE>
 A/Cross-references: UNIPROT:P42081; GB:L25259; NID:G416368; PIDN:AAA58389.1; PID:G416369
 A/Note: It is uncertain whether Met-1 or Met-7 is the initiator
 R/Azuma, M.; Ito, D.; Yagita, H.; Okumura, K.; Phillips, J.H.; Lanier, L.L.; Somoza, C.
 Nature 366, 76-79, 1993
 A/Title: B70 antigen is a second ligand for CTLA-4 and CD28.
 A/Reference number: S39055; MUID:94050123; PMID:7694153
 A/Accession: S39055
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 7-329 <AZU>
 A/Cross-references: GB:U04343; NID:G439838; PIDN:ABA03814.1; PID:G439839
 C/Genetics:
 A/Gene: GDB:CD86; CD28LG2
 A/Cross-references: GDB:433597; OMIM:601020
 A/Map position: 3q13.3-3q21
 C/Superfamily: B7-2 antigen
 C/Keywords: glycoprotein

Query Match 3.0%; Score 10; DB 1; Length 329;
 Best Local Similarity 100.0%; Pred. No. 0.049;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLSNILFVM 10

RESULT 5

CD86 precursor - rabbit
 C/Species: Oryctolagus cuniculus (domestic rabbit)
 C/Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004
 C/Accession: I46691
 R/Isono, T.; Sato, A.
 Immunogenetics 42, 217-220, 1995
 A/Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecule
 A/Reference number: I46689; MUID:9536849; PMID:7642234
 A/Accession: I46691
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-330 <ISO>
 A/Cross-references: UNIPROT:P42071; GB:I49842; NID:G755098; PIDN:BA08642.1; PID:G75509
 C/Superfamily: B7-2 antigen

Query Match 3.0%; Score 10; DB 2; Length 330;
 Best Local Similarity 100.0%; Pred. No. 0.05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 91 LHNVOIKDKG 100

Db 97 LHNVOIKDKG 106

RESULT 6
 S74562
 hypothetical protein s110224 - Synechocystis sp. (strain PCC 6803)
 C/Species: Synechocystis sp.
 A/Variety: PCC 6803
 C/Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
 C/Accession: S74562
 R/Kanehisa, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asanizu, E.; Nakamura, Y.; Miyajima, N.
 O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996
 A/Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
 A/Reference number: S74322; MUID:97061201; PMID:8905231
 A/Accession: S74562
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-298 <KAN>
 A/Cross-references: UNIPROT:P72707; EMBL:D90900; GB:AB001339; NID:G1651768; PIDN:BA0167
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 2.4%; Score 8; DB 2; Length 298;
 Best Local Similarity 100.0%; Pred. No. 5.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 LLSGASL 20

Db 12 LLSGASL 19

RESULT 7
 S60967
 YCP1 protein precursor - yeast (Saccharomyces cerevisiae)
 N/Alternate names: glycoprotein 38; protein N171; protein YNL16W
 C/Species: Saccharomyces cerevisiae
 C/Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
 C/Accession: S60967; A56542; S63112; S63814; S33203
 R/Naar, F.; Becam, A.M.; Herbert, C.J.
 submitted to the EMBL Data Library, October 1995
 A/Description: The sequence of 36.8 kb from the left arm of chromosome XIV reveals 24 c
 tonic dystrophy kinase.
 A/Reference number: S60958
 A/Accession: S60967
 A/Molecule type: DNA
 A/Residues: 1-354 <NAS>
 A/Cross-references: UNIPROT:P38616; EMBL:X92517; NID:G1050783; PID:G1050792
 R/Destruelle, M.; Holzer, H.; Klionsky, D.J.

Mo1. Cell. Biol. 14, 2740-2754, 1994
 A>Title: Identification and characterization of a novel yeast gene: the YGP1 gene product
 A/Reference number: A56542; MUID:94187744; PMID:8139573
 A/Accession: A56542
 A>Status: Preliminary
 A/Molecule type: DNA
 A/Residues: 1-46, 'D', '48-78', 'R', '80-354' <DE>
 A/Cross-references: GB:X73030; NID:9297484; PIDN:CAA51513.1; PID:9297485
 A/Note: authors translated the codon ACT for residue 225 as Trp
 R/Narr: F., Becam, A.M., Herbert, C.
 Submitted to the Protein Sequence Database, April 1996
 A/Reference number: S62967
 A/Accession: S63112
 A/Molecule type: DNA
 A/Residues: 1-354 <NMF>
 A/Cross-references: EMBL:Z71436; NID:G1302125; PID:6239816; PID:G1302126; MIPS:YNL160W
 A/Experimental source: strain S286C
 R/Narr: F., Becam, A.M., Herbert, C.J.
 Yeast 12, 169-175, 1996
 A>Title: The sequence of 36.8 kb from the left arm of chromosome XIV reveals 24 complete
 dystrichy kinase.
 A/Reference number: S63805; MUID:96287653; PMID:8686380
 A/Accession: S63814
 A>Status: nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-354 <NMF>
 A/Cross-references: EMBL:X92517; NID:G1050783; PIDN:CAA63279.1; PID:G1050792
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995
 C/Genetics:
 A/Gene: SGD:YGP1
 A/Cross-references: SGD:S0005104; MIPS:YNL160W
 A/Map position: 14L
 C/Keywords: glycoprotein
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-354/Product: YGP1 protein #status predicted <MAT>

Query Match 2.4%; Score 8; DB 2; Length 354;
 Best Local Similarity 100.0%; Pred. No. 6.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 186 NITELYNV 193
 |||||
 Db 106 NITELYNV 113

RESULT 8
 S48394
 probable membrane protein YIL140W - yeast (Saccharomyces cerevisiae)
 C/Species: Saccharomyces cerevisiae
 C/Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 05-Jul-2004
 C/Accession: S48394; S50276
 R/Churcher, C.
 Submitted to the EMBL Data Library, September 1994
 A/Reference number: S48310
 A/Accession: S48394
 A/Molecule type: DNA
 A/Residues: 1-823 <CHD>
 A/Cross-references: UNIPROT:P38928; GB:Z47047; EMBL:Z38059; NID:G603997; PID:G763206; MI
 R/Torpey, L.E.; Gibbs, P.E.W.; Nelson, J.; Lawrence, C.W.
 Yeast 10, 1503-1509, 1994
 A>Title: Cloning and sequence of REV7, a gene whose function is required for DNA damage-
 A/Reference number: S50275; MUID:95176709; PMID:7871890
 A/Accession: S50276
 A>Status: nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 80-823 <TOR>
 A/Cross-references: EMBL:U07228; NID:G460247; PIDN:AA67919.1; PID:G460249
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1994
 C/Genetics:
 A/Gene: SGD:SR04
 A/Cross-references: SGD:S0001402; MIPS:YIL140W
 A/Map position: 9L
 C/Superfamily: Saccharomyces cerevisiae probable membrane protein YIL140W

C/Keywords: transmembrane protein
 F:6-22/Domain: transmembrane #status predicted <TM>
 F:511-527/Domain: transmembrane #status predicted <TM2>

Query Match 2.4%; Score 8; DB 2; Length 823;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 AKPPVQPP 238
 |||||
 Db 633 AKPPVQPP 640

RESULT 9
 138418
 HLA-A2 - human (fragment)
 N/Alternate names: HLA-A23
 C/Species: Homo sapiens (man)
 C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
 C/Accession: 138418, 138419
 R/Balas, A.; Garcia-Sanchez, F.; Gomez-Reino, F.; Vicario, J.L.
 Hum. Immunol. 41, 69-73, 1994
 A>Title: HLA class I allele (HLA-A2) expression defect associated with a mutation in its
 A/Reference number: 138417; MUID:95137784; PMID:7836067
 A/Accession: 138418
 A>Status: Preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-20 <RES>
 A/Cross-references: UNIPROT:P01892; UNIPROT:O19620; EMBL:U02935; NID:G414545; PIDN:AAA7
 A/Accession: 138419
 A>Status: Preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-20 <RES>
 A/Cross-references: EMBL:U02936; NID:G414547; PIDN:AAA76609.1; PID:G414548
 A/Molecule type: DNA
 A/Residues: 1-20 <RES>
 A/Cross-references: EMBL:U02936; NID:G414547; PIDN:AAA76609.1; PID:G414548
 A/Map position: 6p21.3
 C/Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 2.1%; Score 7; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.3;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VLLSGA 17
 |||||
 Db 10 VLLSGA 16

RESULT 10
 A48972
 mannose-specific lectin - ramson (fragment)
 C/Species: Allium ursinum (ramson)
 C/Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 28-Apr-1995
 C/Accession: A48972
 R/Kaku, H.; Goldstein, I.J.; Van Damme, E.J.; Peumans, W.J.
 Carbohydr. Res. 229, 347-353, 1992
 A>Title: New mannose-specific lectins from garlic (Allium sativum) and ramsons (Allium
 A/Reference number: A48972; MUID:93008079; PMID:1394291
 A/Accession: A48972
 A>Status: Preliminary
 A/Molecule type: protein
 A/Residues: 1-34 <KAK>
 A/Experimental source: bulb
 A/Note: sequence extracted from NCBI backbone (NCBI:P:119584)

Query Match 2.1%; Score 7; DB 2; Length 34;
 Best Local Similarity 100.0%; Pred. No. 8.4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 DNLVLYE 61
 |||||
 Db 28 DNLVLYE 34

RESULT 11
S39376
lectin - shallot
C:Species: Allium ascalonicum (shallot)
C:Date: 19-May-1994 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C:Accession: S39376
R:Mo, H.; van Damme, E.J.M.; Peumans, W.J.; Goldstein, I.J.
Arch. Biochem. Biophys. 306, 431-438, 1993
A:Title: Purification and characterization of a mannose-specific lectin from shallot (A1
A:Reference number: S39376; MUID:94029015; PMID:8215447
A:Accession: S39376
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-38 <MO>
A:Cross-references: UNIPROT:Q9S8Q9

Query Match
Best Local Similarity 2.1%; Score 7; DB 2; Length 38;
100.0%; Pred. No. 9.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 DNLVLYE 61
|||||
Db 29 DNLVLYE 35

RESULT 12
W7WU
E7 protein - human papillomavirus type 1a
C:Species: human papillomavirus type 1a
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C:Accession: C17475
R:Danos, O.; Karinka, M.; Yaniv, M.
EMBO J. 1, 231-236, 1982
A:Title: Human papillomavirus 1a complete DNA sequence: a novel type of genome organization
A:Reference number: A90970; MUID:84182467; PMID:6325156
A:Accession: C17475
A:Molecule type: DNA
A:Residues: 1-93 <DN>
A:Cross-references: UNIPROT:P06465; GB:V01116; GB:X03321; NID:g60966; PIDN:CAA24316.1; F
R:Danos, O.; Engel, L.W.; Chen, B.Y.; Yaniv, M.; Howley, P.M.
J. Virol. 46, 557-566, 1983
A:Title: Comparative analysis of the human type 1a and bovine type 1 papillomavirus gene
A:Reference number: A92993; MUID:83189357; PMID:6302319
A:Contents: annotation
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation

Query Match
Best Local Similarity 2.1%; Score 7; DB 1; Length 93;
100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 212 VQLLEPS 218
|||||
Db 12 VQLLEPS 18

RESULT 13
G90536
hypothetical protein MYPU 1990 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C:Species: Mycoplasma pulmonis
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: G90536
R:Hamoud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Gallison, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A:Reference number: A95512; MUID:21267165; PMID:11353084
A:Accession: G90536
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-101 <KUR>
A:Cross-references: UNIPROT:Q98H11; GB:AL445566; PID:g14089612; PIDN:CAC13372.1; GSPDB:G
A:Experimental source: strain UAB CTIP

C:Genetics:
A:Gene: MYPU 1990
A:Genetic code: SGC3

Query Match
Best Local Similarity 2.1%; Score 7; DB 2; Length 101;
100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 LINTKNS 172
|||||
Db 81 LINTKNS 87

RESULT 14
E75616
hypothetical protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: E75616
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: E75616
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-135 <WHI>
A:Cross-references: UNIPROT:Q9RYV9; GB:AE001862; GB:AE001825; NID:g6460468; PIDN:AAF123
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR0197
A:Map position: 2

Query Match
Best Local Similarity 2.1%; Score 7; DB 2; Length 135;
100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VLLSGA 17
|||||
Db 17 VLLSGA 23

RESULT 15
F75327
hypothetical protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: F75327
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: F75327
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-149 <WHI>
A:Cross-references: UNIPROT:Q9RSV4; GB:AE002038; GB:AE000513; NID:g6459790; PIDN:AAF115
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR2018
A:Map position: 1

Query Match
Best Local Similarity 2.1%; Score 7; DB 2; Length 149;
100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LILSGA 18
|||||
Db 47 LILSGA 53

Thu Dec 16 12:21:14 2004

us-09-868-605-14.Oligo.rpr

Page 5

Search completed: December 15, 2004, 17:01:04
Job time : 42 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 15, 2004, 16:38:47 ; Search time 196 Seconds
(without alignments)
968.743 Million cell updates/sec

Title: US-09-868-605-14
Perfect score: 330
Sequence: 1 MGSLNLFVWVLLSGAASL.....NLTASDNDSTDFLAKSL 330

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1825181 seqs, 575374646 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database : uniprot_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	325	98.5	325	2	002838 sus scrofa
2	44	13.3	44	2	096KJ5 sus scrofa
3	19	5.8	93	2	06QW20 bos taurus
4	19	5.8	93	2	AAS48374 Aas48374 bos tauru
5	19	5.8	284	2	09GLJ3 09GLJ3 bos taurus
6	14	4.2	329	2	09XGX6 09XGX6 felis silve
7	14	4.2	332	2	09GWM7 09GWM7 felis silve
8	14	4.2	332	2	09SL16 09SL16 felis silve
9	13	3.9	280	2	09TTF1 09TTF1 canis famli
10	13	3.9	329	2	09TTF2 09TTF2 canis famli
11	12	3.6	309	1	CD86_MOUSE P42082 mus musculu
12	12	3.6	309	2	091YV7 091YV7 mus musculu
13	12	3.6	309	2	AAD25880 AAD25880 mus muscu
14	12	3.6	309	2	AAD25881 AAD25881 mus muscu
15	12	3.6	309	2	AAD25882 AAD25882 mus muscu
16	12	3.6	309	2	AAD25883 AAD25883 mus muscu
17	12	3.6	309	2	BAC37666 BAC37666 mus muscu
18	12	3.6	314	2	061238 061238 mus musculu
19	12	3.6	356	2	064381 064381 mus musculu
20	10	3.0	149	2	062810 062810 rattus norv
21	10	3.0	275	2	09BDN9 09BDN9 papio anubi
22	10	3.0	313	2	035531 035531 rattus norv
23	10	3.0	323	2	09BD88 09BD88 cervocobus
24	10	3.0	323	2	09BDM2 09BDM2 cervocoplhec
25	10	3.0	323	2	09BDM4 09BDM4 macaca mula
26	10	3.0	323	2	09BDM9 09BDM9 macaca neme
27	10	3.0	329	1	CD86_HUMAN P42081 homo sapien
28	10	3.0	329	1	AHA40261 AHA40261 homo sapi
29	10	3.0	329	1	CD86_RABIT P42071 coryctolagus
30	10	3.0	329	1	CD86_RABIT P42071 coryctolagus
31	8	2.4	108	2	08Y224 08Y224 ralestona s
	8	2.4	250	2	088Y46 088Y46 lactobacill

ALIGNMENTS

ID	002838	PRELIMINARY;	PRT;	325 AA.
AC	002838.			
DI	01-UTL-1997 (TREMBlrel. 04, Created)			
DT	01-UTL-1997 (TREMBlrel. 04, Last sequence update)			
DT	01-OCT-2003 (TREMBlrel. 25, Last annotation update)			
DE	B7-2.			
GN	Name=CD86;			
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.			
OX	NCB1_taxid=9623;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97047772; PubMed=8892613;			
RA	Maher S.E., Karmann K., Min W., Hughes C.C., Pober J.S.,			
RA	Bothwell A.L.;			
RT	"Porcine endothelial CD86 is a major costimulator of xenogeneic human			
RT	T cells: cloning, sequencing, and functional expression in human			
RT	endothelial cells."			
RL	J. Immunol. 157:3838-3844(1996).			
DR	EMBL; L76039; AAB61307.1; -.			
DR	HSSP; P42081; INCN			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003596; IG_v.			
DR	Pfam; PF00047; IG_1.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG_Like; 1.			
SQ	SEQUENCE 325 AA; 36527 MW; 98880813780597D CRC64;			
Query Match 98.5%; Score 325; DB 2; Length 325;				
Best local Similarity 100.0%; Pred. No. 0;				
Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1	MGSLNLFVWVLLSGAASLKSQAYFNETGELPCHFTNSQNLSDLVIFWQDDNVLVLY	60	
DB	1	MGSLNLFVWVLLSGAASLKSQAYFNETGELPCHFTNSQNLSDLVIFWQDDNVLVLY	60	
QY	61	ELYRGOEKPHNVNSKYNRISFDQATWTLRLHNVQIQDKSGYQCFIHKKPHGGLVPIHOM	120	
DB	61	ELYRGOEKPHNVNSKYNRISFDQATWTLRLHNVQIQDKSGYQCFIHKKPHGGLVPIHOM	120	
QY	121	SSDSLILANFQPEINILNHTENSVINLTCSSTOGYPEPORMMLANTKUSTEHADAM	180	
DB	121	SSDSLILANFQPEINILNHTENSVINLTCSSTOGYPEPORMMLANTKUSTEHADAM	180	
QY	181	KKSONNITELYNVSIKPLIPETNVSIVCVQLQESKTLFSLPCNIDAKPPVQPPVP	240	
DB	181	KKSONNITELYNVSIKPLIPETNVSIVCVQLQESKTLFSLPCNIDAKPPVQPPVP	240	
QY	241	DIHIMIALVTVVVGWMSFVTLRKKKKOPSPNECGFTIKMKKASQITKRAEVH	300	
DB	241	DIHIMIALVTVVVGWMSFVTLRKKKKOPSPNECGFTIKMKKASQITKRAEVH	300	

QY 301 ERSDDAQCQVNIKLTASPDNSTTDF 325
 DB 301 ERSDDAQCQVNIKLTASPDNSTTDF 325

RESULT 2

Q9GKJ5 PRELIMINARY; PRT; 44 AA.
 AC Q9GKJ5;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE Cosmimulatory B-lymphocyte antigen B7-2 (Fragment).
 GN Name=CD86; (Pig).
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9913;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21419000; PubMed=11528129;
 RA Van Poucke M., Verle M., Tuglie C., Piumi F., Genet C.,
 RA Van Zeveren A., Peelman L.J.;
 RT "Integration of porcine chromosome 13 maps."
 RL Cytogenet. Cell Genet. 93:297-303(2001).
 DR EMBL; AF222915; AAG41128.1; --
 FT NON TER 1
 FT NON TER 44
 SQ SEQUENCE 44 AA; 5172 MW; 0721760B21759C CRC64;

Query Match 13.3%; Score 44; DB 2; Length 44;
 Best Local Similarity 100.0%; Pred. No. 4.7e-16;
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 157 YPEPQRMVLTNKTSTTEHDADKKSONNITELYNSIRSLP 200
 DB 1 YPEPQRMVLTNKTSTTEHDADKKSONNITELYNSIRSLP 44

RESULT 3

Q6QM20 PRELIMINARY; PRT; 93 AA.
 AC Q6QM20;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE CD86 (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Norimine J., Brown W.C.;
 RL Submitted (Jan-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF533858; AAS48374.1; --
 FT NON TER 1
 FT NON TER 93
 SQ SEQUENCE 93 AA; 10281 MW; 323B38A28889D6C3 CRC64;

Query Match 5.8%; Score 19; DB 2; Length 93;
 Best Local Similarity 100.0%; Pred. No. 1.4e-10;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 PPVPDHIIIMIALVTVV 255
 DB 6 PPVPDHIIIMIALVTVV 24

RESULT 4
 AAS48374 PRELIMINARY; PRT; 93 AA.
 ID AAS48374

AC AAS48374;
 DT 10-MAR-2004 (TREMBLrel. 27, Created)
 DT 10-MAR-2004 (TREMBLrel. 27, Last sequence update)
 DT 10-MAR-2004 (TREMBLrel. 27, Last annotation update)
 DE CD86 (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Norimine J., Brown W.C.;
 RT "Bovine CD86 3' UTR."
 RL Submitted (Jan-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF533858; AAS48374.1; --
 FT NON TER 1
 FT NON TER 284
 SQ SEQUENCE 93 AA; 10281 MW; 323B38A28889D6C3 CRC64;

Query Match 5.8%; Score 19; DB 2; Length 93;
 Best Local Similarity 100.0%; Pred. No. 1.4e-10;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 PPVPDHIIIMIALVTVV 255
 DB 6 PPVPDHIIIMIALVTVV 24

RESULT 5
 Q9GLJ3 PRELIMINARY; PRT; 284 AA.
 AC Q9GLJ3;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE CD86 antigen (Fragment).
 GN Name=CD86;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Tissue=Peripheral blood;
 RA Brooke G.P., Howard C.J., Parsons K.R.;
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ291475; CAC13140.1; --
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON TER 284
 FT NON TER 284
 SQ SEQUENCE 284 AA; 32021 MW; 797BB6639E297841 CRC64;

Query Match 5.8%; Score 19; DB 2; Length 284;
 Best Local Similarity 100.0%; Pred. No. 3.7e-10;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 PPVPDHIIIMIALVTVV 255
 DB 251 PPVPDHIIIMIALVTVV 269

RESULT 6
 Q9XSX6 PRELIMINARY; PRT; 329 AA.
 ID Q9XSX6
 AC Q9XSX6;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE CD86 antigen.

GN Name=CD86;
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCB1_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20180222; PubMed=10711336;
 RA Choi I.S., Hash S.M., Winslow B.J., Collisson E.W.;
 RT "Sequence analyses of feline B7 costimulatory molecules.";
 RL Vet. Immunol. Immunopathol. 73:219-231(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Choi I.S., Hash S., Winslow B.J., Collisson E.W.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF157827; RAD42974.1; -.
 DR HSSP: P42081; INCN.
 DR InterPro: IPR007110; Ig-like.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 SQ SEQUENCE 329 AA; 37481 MW; A10621E3C00A08BB CRC64;

Query Match 4.2%; Score 14; DB 2; Length 329;
 Best Local Similarity 100.0%; Pred. No. 4.7e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 WTLLRHNVQIKDKG 100
 DB 94 WTLLRHNVQIKDKG 107

RESULT 7
 ID 09GMZ7 PRELIMINARY; PRT; 332 AA.
 AC 09GMZ7;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE B-lymphocyte activation antigen B7-2 (CD86).
 OS Name=CD86;
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCB1_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20485322; PubMed=11029611;
 RA Mishimura Y., Shimojima M., Miyazawa T., Sato E., Nakamura K.,
 RA Isumiya Y., Ikeda Y., Mikami T., Takahashi E.;
 RT "Molecular cloning of the cDNA encoding the feline B-lymphocyte
 RT interaction antigen B7-1 (CD80) and B7-2 (CD86) homologues which
 RT interact with human CTLA4-1g.";
 RL Eur. J. Immunogenet. 27:427-430(2000).
 DR EMBL: AB030652; BAB11688.1; -.
 DR HSSP: P42081; INCN.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; IG_V.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 SQ SEQUENCE 332 AA; 37812 MW; 672C8B367D1E3C0 CRC64;

Query Match 4.2%; Score 14; DB 2; Length 332;
 Best Local Similarity 100.0%; Pred. No. 4.7e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 WTLLRHNVQIKDKG 100
 DB 94 WTLLRHNVQIKDKG 107

RESULT 8
 Q95L16

ID 095L16 PRELIMINARY; PRT; 332 AA.
 AC 095L16;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE CD86.
 GN Name=CD86;
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCB1_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21390213; PubMed=11498243;
 RA Yang S., Sellins K.S., Powell T., Stoneman E., Sim G.K.;
 RT "Novel transcripts encoding secreted forms of feline CD80 and CD86
 RT costimulatory molecules.";
 RL Vet. Immunol. Immunopathol. 81:15-21(2001).
 DR EMBL: AY007704; AAG23342.1; -.
 DR HSSP: P42081; INCN.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; IG_V.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 SQ SEQUENCE 332 AA; 37826 MW; 8BFC8B367D1E3D8 CRC64;

Query Match 4.2%; Score 14; DB 2; Length 332;
 Best Local Similarity 100.0%; Pred. No. 4.7e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 WTLLRHNVQIKDKG 100
 DB 94 WTLLRHNVQIKDKG 107

RESULT 9
 ID 09TFL1 PRELIMINARY; PRT; 280 AA.
 AC 09TFL1;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Truncated B7-2 protein.
 GN Name=CD86;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCB1_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20093996; PubMed=10630300;
 RA Yang S., Sim G.K.,
 RT "New forms of dog CD80 and CD86 transcripts that encode secreted B7
 RT molecules.";
 RL Immunogenetics 50:349-353(1999).
 DR EMBL: AF106827; AAF17298.1; -.
 DR HSSP: P42081; INCN.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN 1.
 SQ SEQUENCE 280 AA; 32265 MW; 3C8BCA4D826A7F3 CRC64;

Query Match 3.9%; Score 13; DB 2; Length 280;
 Best Local Similarity 100.0%; Pred. No. 0.0004;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 TGEPLCHFTNSQN 41
 DB 35 TGEPLCHFTNSQN 47

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RESULT 10
Q9TF2 PRELIMINARY; PRT; 329 AA.
AC Q9TF2;
ID Q9TF2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2004 (TREMBLrel. 26, Last annotation update)
DE B7-2 protein.
GN Name=CD86;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2009396; PubMed=10630300;
RA Yang S., Sim G.-K.;
RT "New forms of dog CD80 and CD86 transcripts that encode secreted B7
RT molecules."
RL Immunogenetics 50:349-353(1999).
DR EMBL; AF106825; AAF17297.1; -.
DR HSP; P42081; INCN.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN; 1.
SQ SEQUENCE 329 AA; 37774 MW; D98B83437B7B73 CRC64;

Query Match 3.9%; Score 13; DB 2; Length 329;
Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 TGELEPCHTNSCN 41
Db 35 TGELEPCHTNSCN 47

RESULT 11
CD86_MOUSE STANDARD; PRT; 309 AA.
ID CD86_MOUSE
AC P42082;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE T lymphocyte activation antigen CD86 precursor (Activation B7-2
DE antigen) (Early T cell costimulatory molecule-1) (ETC-1).
GN Name=CD86;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9405585; PubMed=7504059;
RA Freeman G.J., Borriello F., Hodges R.J., Reiser H., Gibben J.G.,
RA Ng J.W., Kim J., Goldberg J.M., Hathcock K., Lasko G., Lombard L.A.,
RA Wang S., Gray G.S., Nadler L.M., Sharpe A.H.;
RT "Murine B7-2, an alternative CTLA4 counter-receptor that costimulates
RT T cell proliferation and interleukin 2 production."
RL J. Exp. Med. 178:2185-2192(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RA MEDLINE=96094437; PubMed=7499829;
RA Borriello F., Oliveros J., Freeman G.J., Nadler L.M., Sharpe A.H.;
RT "Differential expression of alternate mB7-2 transcripts."
RL J. Immunol. 155:5490-5497(1995).
RN [3]
RP SEQUENCE OF 7-309 FROM N.A.
RX MEDLINE=94230971; PubMed=7513726;

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RA Chen C., Gault A., Shen L., Nabavi N.;
RT "Molecular cloning and expression of early T cell costimulatory
RT molecule-1 and its characterization as B7-2 molecule."
RL J. Immunol. 152:4929-4936(1994).
CC -1- FUNCTION: Receptor involved in the costimulatory signal essential
CC for T lymphocyte proliferation and interleukin 2 production, by
CC binding CD28 or CTLA-4. May play a critical role in the early
CC events of T cell activation and costimulation of naive T cells,
CC such as deciding between immunity and anergy that is made by T
CC cells within 24 hours after activation.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed on activated B cells.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -1- CAUTION: It is uncertain whether Met-1 or Met-7 is the initiator.
CC
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
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CC or send an email to license@sib-sib.ch).
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QY 87 WTLRLHNVQIKD 98
 DB 93 WTLRLHNVQIKD 104

RESULT 12

Q91YV7 PRELIMINARY; PRT; 309 AA.
 AC Q91YV7
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
 DE CD86 antigen.
 GN Name=CD86;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
 RC Expression driven by an MMTV-LTR enhancer;
 RX MEDLINE=22388257; PubMed=1247932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Martusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Donald W.F., Caesvant T.L., Scheetz T.E.,
 RA Brownstein M.U., Ussid T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millan S.J.,
 RA Bosak S.A., Mcwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy U., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalski U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
 RC Expression driven by an MMTV-LTR enhancer;
 RA Strausberg R., et al. (2001) to the EMBL/GenBank/DBJ databases.
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC013807; AAH13807.1; -
 DR HSSP; P42081; INCN.
 DR MGD; MGI:101773; Cd86.
 DR GO; GO:0009897; C:external side of plasma membrane; IDA.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_V.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LINK; 1.
 SQ SEQUENCE 309 AA; 34713 MW; 61593C49FCB0C5 CRC64;

Query Match 3.6%; Score 12; DB 2; Length 309;
 Best Local Similarity 100.0%; Pred. No. 0.0045;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 WTLRLHNVQIKD 98
 DB 93 WTLRLHNVQIKD 104

RESULT 13

AAD25880

ID AAD25880 PRELIMINARY; PRT; 309 AA.

AC AAD25880
 DT 02-MAR-2004 (TREMblrel. 27, Created)
 DT 02-MAR-2004 (TREMblrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMblrel. 27, Last annotation update)
 DE CD86 antigen.
 GN CD86.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A/J; TISSUE=spleen;
 RA Ma R.Z., Teuscher C.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF065897; AAD25880.1; -
 SQ SEQUENCE 309 AA; 34665 MW; 8F58DCD1FB81D5EA CRC64;

Query Match 3.6%; Score 12; DB 2; Length 309;
 Best Local Similarity 100.0%; Pred. No. 0.0045;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 WTLRLHNVQIKD 98
 DB 93 WTLRLHNVQIKD 104

RESULT 14

AAD25881 PRELIMINARY; PRT; 309 AA.
 AC AAD25881
 DT 02-MAR-2004 (TREMblrel. 27, Created)
 DT 02-MAR-2004 (TREMblrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMblrel. 27, Last annotation update)
 DE CD86 antigen.
 GN CD86.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=spleen;
 RA Ma R.Z., Teuscher C.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF065898; AAD25881.1; -
 SQ SEQUENCE 309 AA; 34665 MW; 8F58DCD1FB81D5EA CRC64;

Query Match 3.6%; Score 12; DB 2; Length 309;
 Best Local Similarity 100.0%; Pred. No. 0.0045;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 WTLRLHNVQIKD 98
 DB 93 WTLRLHNVQIKD 104

RESULT 15

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 DT 02-MAR-2004 (TREMblrel. 27, Created)
 DT 02-MAR-2004 (TREMblrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMblrel. 27, Last annotation update)
 DE CD86 antigen.
 GN CD86.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=B10.S/J; TISSUE=spleen;
 RA Ma R 2, Teuscher C; to the EMBL/GenBank/DBJ databases.
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF065899; AAD25882.1; -
 SQ SEQUENCE 309 AA; 3465 MW; 8F58DDC1FB81D5EA CRC64;

Query Match 3.6%; Score 12; DB 2; Length 309;
 Best Local Similarity 100.0%; Pred.No. 0.0045;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 87 WTLRLHNVQIKD 98
 |||||
 Db 93 WTLRLHNVQIKD 104

Search completed: December 15, 2004, 17:00:18
 Job time : 199 secs